

[illegible]

CGAGGGGGGACGACCTXCTGCCGACCCCTGCCGGAAGAGGGGGAAAAAGGAGGGGTACGAGGGTGGGGCAICCTG	417
.....C.....G.....C.....G.....	414
.....G.....CG.....	420
.....T.....C.....	
AGCCCCGACCGCCGACCTGTACGCGCTCCCTTCCGAGCGGCAICGGCGTCCCTCCACCCCGACGGGTACCTCA	487
.....AAA.....T.....CA.....	484
.....T.....G.....G.....A.....T.....G.....	490
.....A.....G.....G.....G.....CC.....	
TCGCCCCCGCGTGGCTTGGGAGAGTACGGCCCTGAGCCCGGAGCACTGGGTGGACTACGGGGCGCCCTGGG	557
.....C.....A.....C.....G.....CC.....A.....	554
.....AC.....C.....C.....	560
.....A.....C.....T.....C.....C.....	
GGGGGACCCCTGGGACCACTCCCCGGGTGAAGGGCATCGGGGAGAGACCGCCGCGCAAGCTCGCTCXAG	627
.....GAG.....T.....G.....G.....T.....GG.....	624
.....G.....T.....A.....G.....A.....G.....A.....GG.....	630
.....G.....T.....A.....T.....C.....	
CGCTGGGGGACCCCTGGAAAAAGCTCCTCAAGAACCTGGACGGGGTGAAGCCCGC...CXTCCGGGGACAGAGA	694
.....CG.....G.....A.....A.....	691
.....T.....C.....C.....A.....T.....T.....G.....C.....	700
.....A.....A.....A.....A.....A.....A.....G.....	

SECRET

FIGURE 1D

1114	CGGGCXCTCCTCCCAAGGACCTCCCGCTTTCGGCCCTGAGCGAGGGGCTXGACCTCXTCGGCCGGGACG	1114
1111A.....AG.....G.....A.....T.G.....CG.....G.....	1111
1120G.T.....G.....G.....C.....G.....T.C.....G.A.....G.....	1120
1127AA.....G.....C.....C.....TC.....G.....G.....G.....	1127
1134C.....C.....C.....C.....C.....C.....C.....C.....	1134
1184CCCCATGGTCCCTCCCTGACCTGACCCCTGCACACACCCCGGAGGGGCTGCGCCCGGCTACGG	1184
1181T.....T.....T.....T.....T.....T.....T.....T.....	1181
1190G.....T.....T.....T.....T.....T.....T.....T.....	1190
1254GGGGAGTGGACCGGAGGAXGGGGGGGGAGCGGGGCTCGTCCGAGAGGGCTGTCXGAGACCTXXXGGAG	1254
1251G.....G.....G.....G.....G.....G.....G.....G.....	1251
1260C.....T.....A.....A.....G.....G.....G.....G.....	1260
1267C.....T.....C.....C.....G.....G.....G.....G.....	1267
1324CGCCCTGACGGCGGAGGAGGCTCGTTCGCTTTAGCAGGAGGCTGGACAGGGCCCTTTCGGGGGCTCCTGG	1324
1321G.....G.....G.....G.....G.....G.....G.....G.....	1321
1330A.....A.....A.....A.....A.....A.....A.....A.....	1330
1394CGCCATCGAGGGCCAGCGGGGXCGGGCTGGAGGCTCGCCCTAGCTCCAGGGCCCTXTCCCTGAGGCTGCGCGCA	1394
1391G.....G.....G.....G.....G.....G.....G.....G.....	1391
1400G.....G.....G.....G.....G.....G.....G.....G.....	1400

FIGURE 1E

SEQUENCE	CGAGATCCCGCCCGCTCCAGCAGGAGGCTCTCCGCGCTCCCGCGCGCGCGCGCTCAACCTCAAGCTCCCGCGAG	1464
SEQUENCECC.....	1461
SEQUENCEAG.....	1470
SEQUENCET.....	
SEQUENCE	CAGCTCGAAAGGCTGGCTTTGACCAAGCTXGGGCTCCCGCGCATCGGCAAGACGGAGAGACXGGCAAGC	1534
SEQUENCEA.....	1531
SEQUENCEG.....	1540
SEQUENCETA.....	
SEQUENCE	CGTCCACGAGCGCGCGCGCTCCCTCGAGCGCGCTXGGXGAGCGCGCGCGCGCGCTCGTGGAGAGAGATCGTCCAGTA	1604
SEQUENCEC.....	1601
SEQUENCET.....	1610
SEQUENCEG.....	
SEQUENCE	CGCGCAGCTCACCAGGCTCAAGAGACAGCTAGATXGACCGCGCTGCCXGXCGCTCGTCCACCGCGAGCGCGCG	1674
SEQUENCEG.....	1671
SEQUENCET.....	1680
SEQUENCEG.....	
SEQUENCE	CGCCCTCGACACCGCGCTCAACCGACCGCGCGCGCGCGCGCTAGTACCTCCGACCGCGCAACCTCC	1744
SEQUENCEA.....	1741
SEQUENCEG.....	1750
SEQUENCEC.....	

[REDACTED]

6

FIGURE 1G

SEQUENCE	ACCTCCGCAAGCTCCGCGGCTGGATTGAGAAAGCCGTGGAGGAGGGGAGGAGGGGGGTACCTGGAGA	2164
SEQUENCE	2161
SEQUENCE	2170
SEQUENCE	2174
SEQUENCE	2178
SEQUENCE	2182
SEQUENCE	2186
SEQUENCE	2190
SEQUENCE	2194
SEQUENCE	2198
SEQUENCE	2202
SEQUENCE	2206
SEQUENCE	2210
SEQUENCE	2214
SEQUENCE	2218
SEQUENCE	2222
SEQUENCE	2226
SEQUENCE	2230
SEQUENCE	2234
SEQUENCE	2238
SEQUENCE	2242
SEQUENCE	2246
SEQUENCE	2250
SEQUENCE	2254
SEQUENCE	2258
SEQUENCE	2262
SEQUENCE	2266
SEQUENCE	2270
SEQUENCE	2274
SEQUENCE	2278
SEQUENCE	2282
SEQUENCE	2286
SEQUENCE	2290
SEQUENCE	2294
SEQUENCE	2298
SEQUENCE	2302
SEQUENCE	2306
SEQUENCE	2310
SEQUENCE	2314
SEQUENCE	2318
SEQUENCE	2322
SEQUENCE	2326
SEQUENCE	2330
SEQUENCE	2334
SEQUENCE	2338
SEQUENCE	2342
SEQUENCE	2346
SEQUENCE	2350
SEQUENCE	2354
SEQUENCE	2358
SEQUENCE	2362
SEQUENCE	2366
SEQUENCE	2370
SEQUENCE	2374
SEQUENCE	2378
SEQUENCE	2382
SEQUENCE	2386
SEQUENCE	2390
SEQUENCE	2394
SEQUENCE	2398
SEQUENCE	2402
SEQUENCE	2406
SEQUENCE	2410
SEQUENCE	2414
SEQUENCE	2418
SEQUENCE	2422
SEQUENCE	2426
SEQUENCE	2430
SEQUENCE	2434
SEQUENCE	2438
SEQUENCE	2442
SEQUENCE	2446
SEQUENCE	2450

10033297 110301

7

FIGURE 1H

CCCCCTGCAGCTGCAGGTCCGGATCCGGGAGGCACTCCCTCTCCGGCAGGCACTAG	
.....A.....GA	
.....CC.....GT...	
.....T.....	

2499
2496
2505

[REDACTED]

SECRET

FIGURE 2B

418	417	420	418	487	490	550	557	560	528	527	600	698	697	700
RGUUKOLAVLALREGLOLXPGDDPML LAYLLDPSHTPEGVARYGGEWTEOAGERALLSERLFXKLCXX														
S.....G.P.....E.....A.....A...WG														
I.....F.E.....A.....OT.KE														
S.....V.....AH.....HA..LK														
RIEGEERLLWLYXEVEKPLSAVLAKMEATGVRLDVAYLOALSLEVAEEIRLLEEVEVRLAOGHPFNLSRD														
R.....R.....A.....R.....A.....														
E.....R.....EA.V.O.....														
K.....K.....L.....														
OLERVLFDELGLPAICKTEKTKRSTSAAVLEALAEAPHIVEKILQYRELTKLKHNTYIDPLPXLVMPRTG														
R.....L.....O.....S.....O.I.....														
R.....OR.....H.....V.....S.....														
RLHTRFNQATATGRSSSDPNLOHI PVRTPLQORI RRAFVAEEGWXLVALDYSOIELRVLAHLSODEHL														
R.....L.....L.....V.....V.....														
IRVFOEGROI HTASWNFCVPPEAUDPLMRAAKTINFGVLYGNSAHRLSQELAI PYEEAVAFIERYFO														
E.....R.....G.....S.....														
K.....S.....G.....V.....														

FIGURE 2C

WJORITY	SFPKVRWILEXTLEECRRROYVETLFGARRYPOLNARUKSVREAAERMAFHPVOGTAADLMKLAHVXL	768
WJORITYE.....	767
WJORITYG.....	770
WJORITYK.....	
WJORITY	FPRLEXMGARHLLOVHDEIVLEAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVOXGEDWLSAKEX	
WJORITYE.....A.....R.....	833
WJORITYD.....R.....W.....O.....	831
WJORITYL.....DA.....E.....A.....KA.....	835
WJORITYL.....	
WJORITY	

FIGURE 3

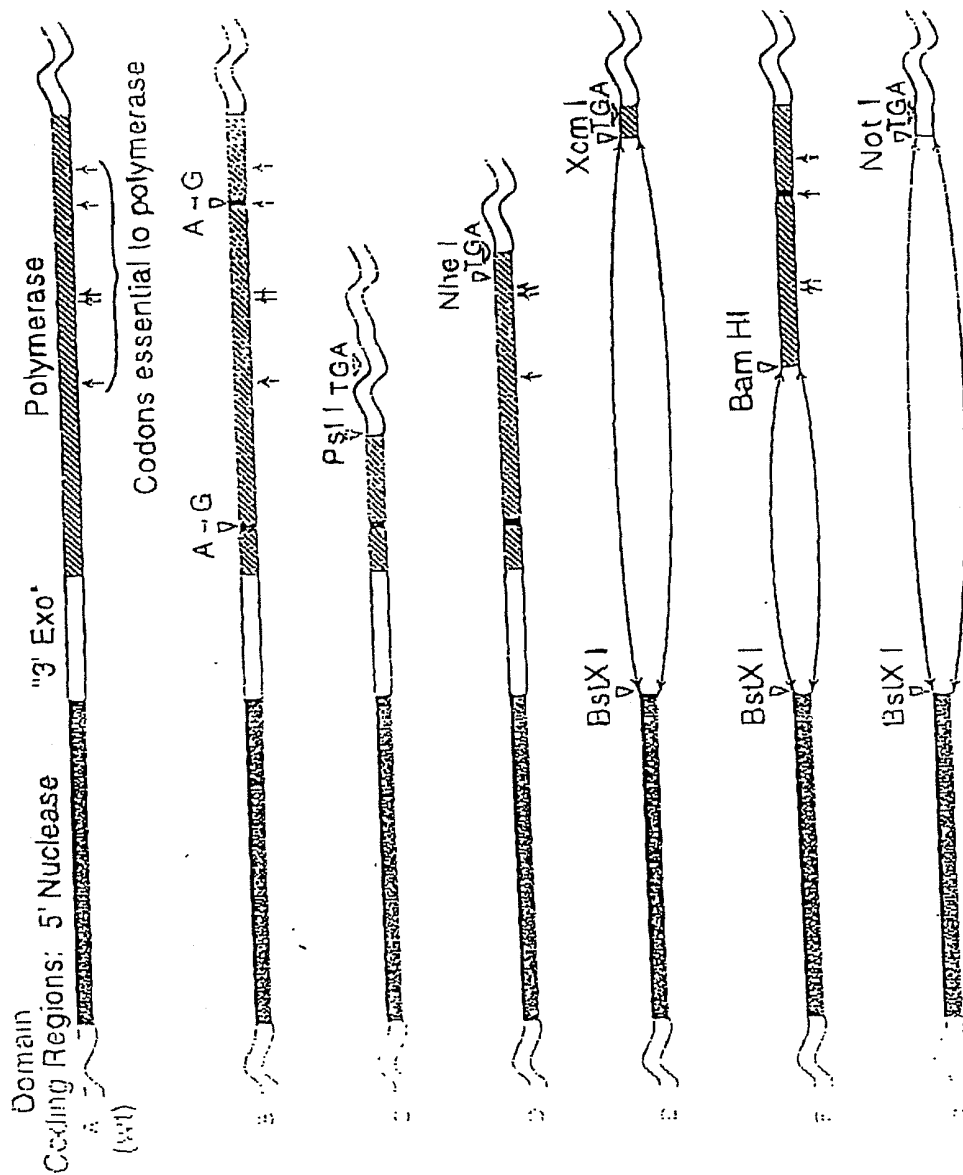


FIGURE 4

Genes for Wild-Type and Pol(-) DNAPTH

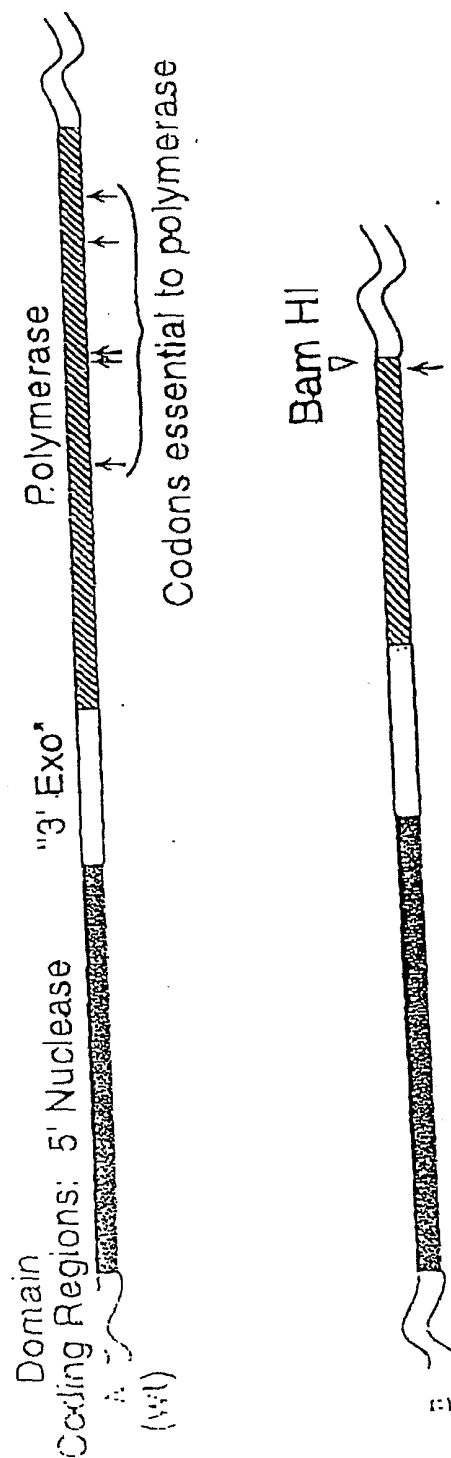
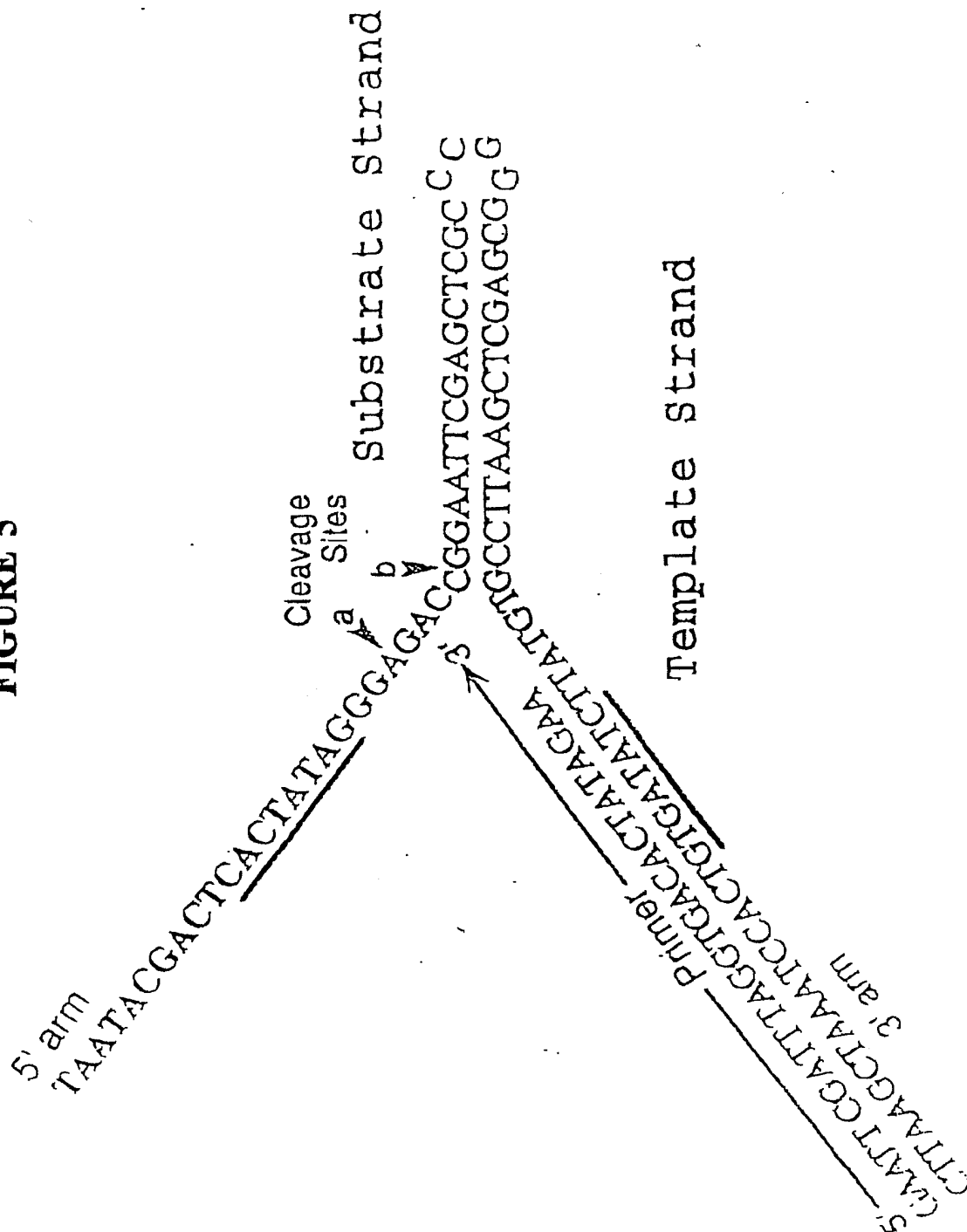


FIGURE 5



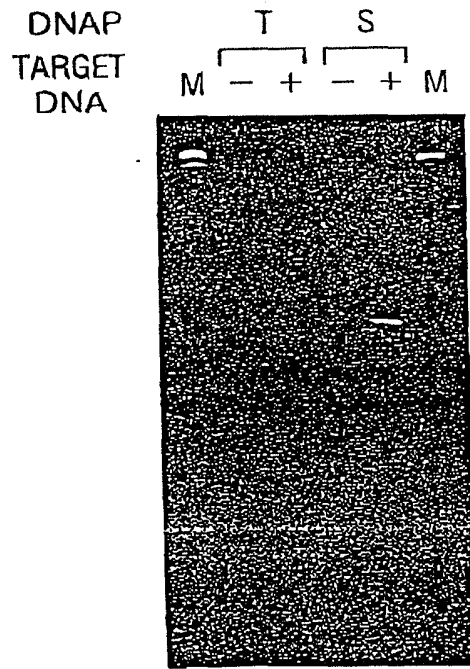


FIGURE 6

15

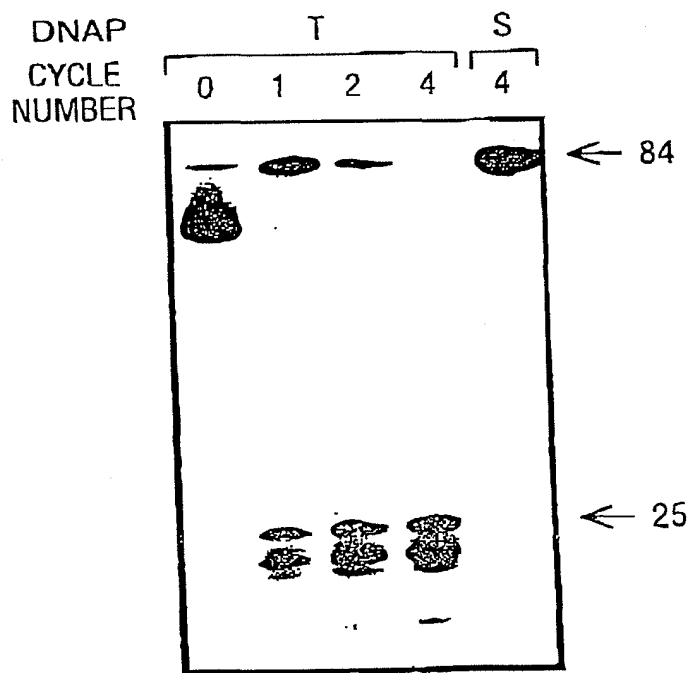


FIGURE 7

17

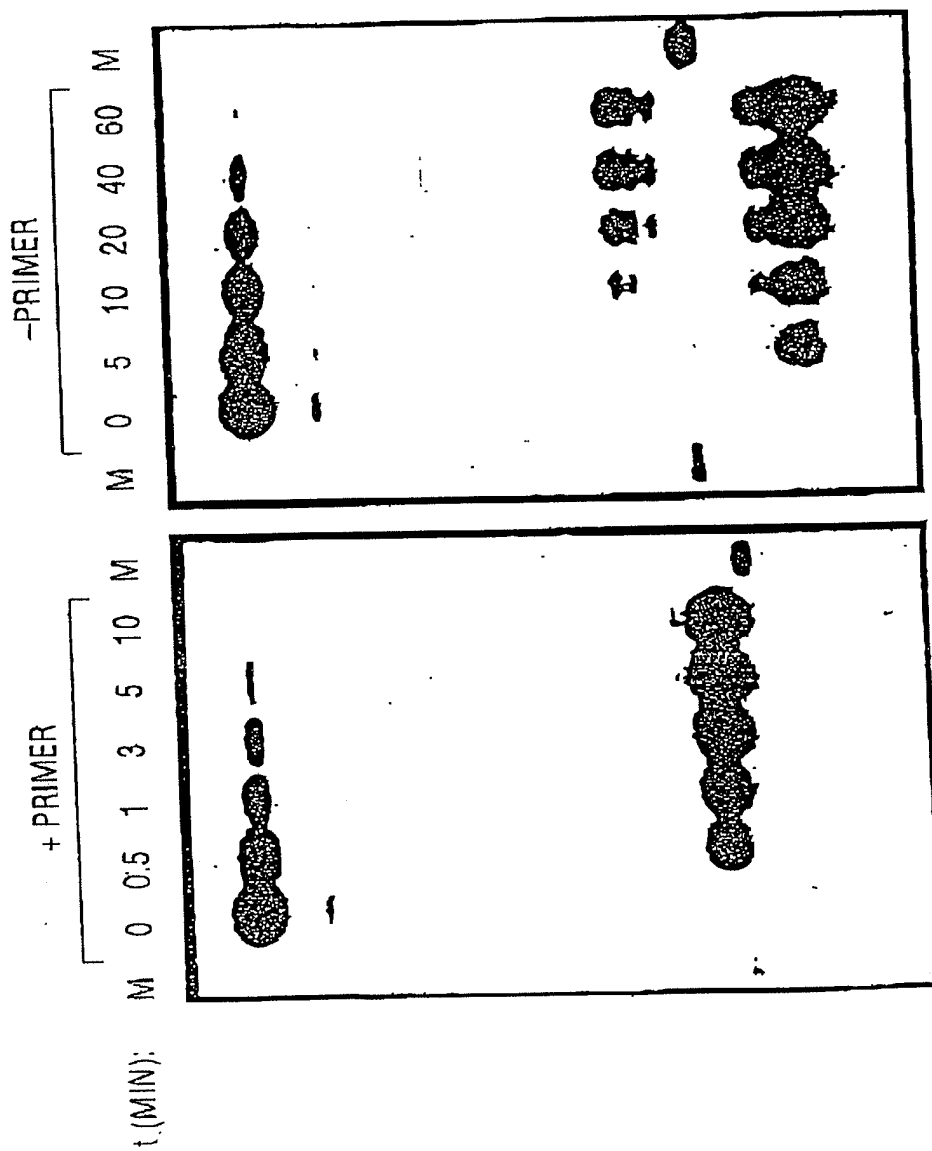


FIGURE 9B

FIGURE 9A

(3)

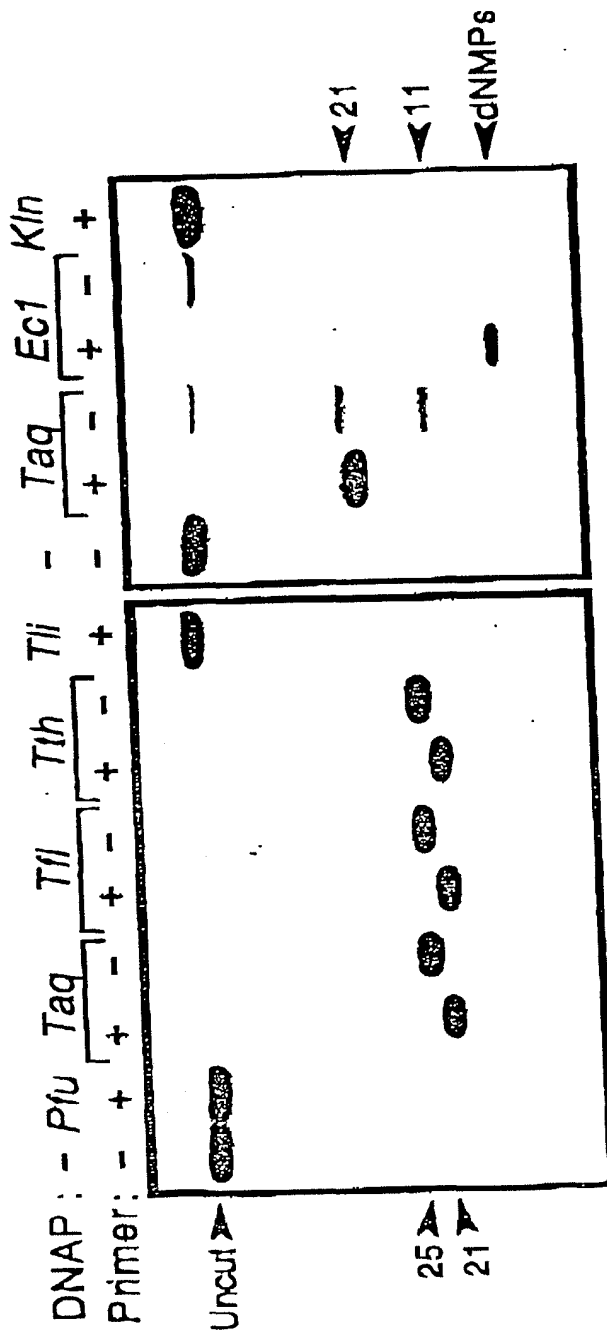
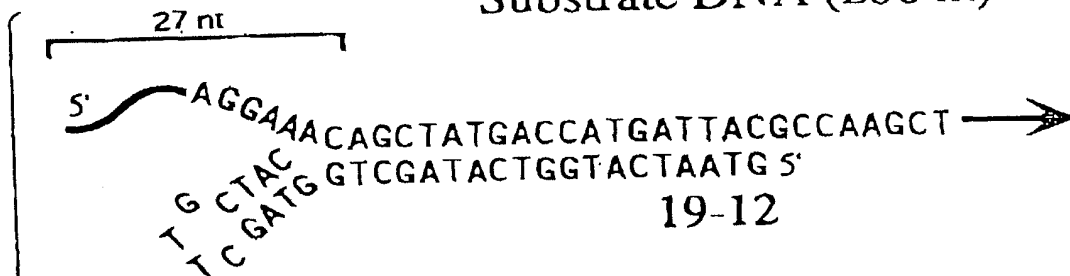


FIGURE 10A

FIGURE 10B

Substrate DNA (206 nt)



Substrate DNA (206 nt)

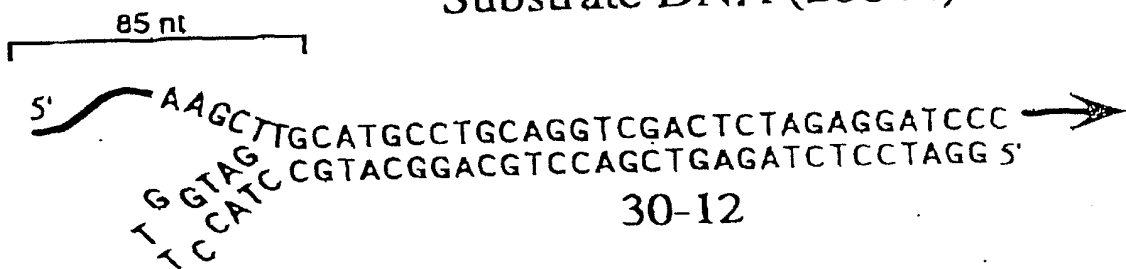


FIGURE 11A

Substrate RNA (46 nt)

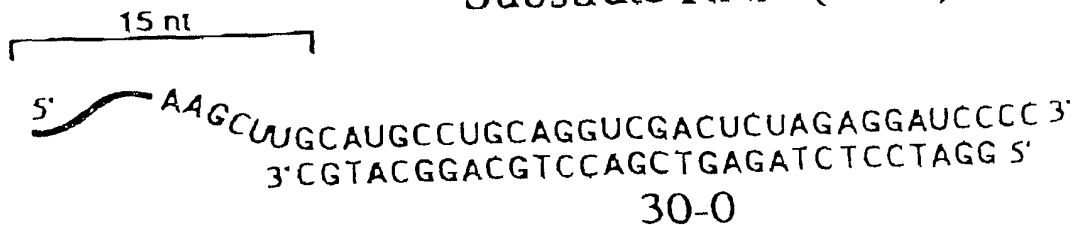


FIGURE 12A

20

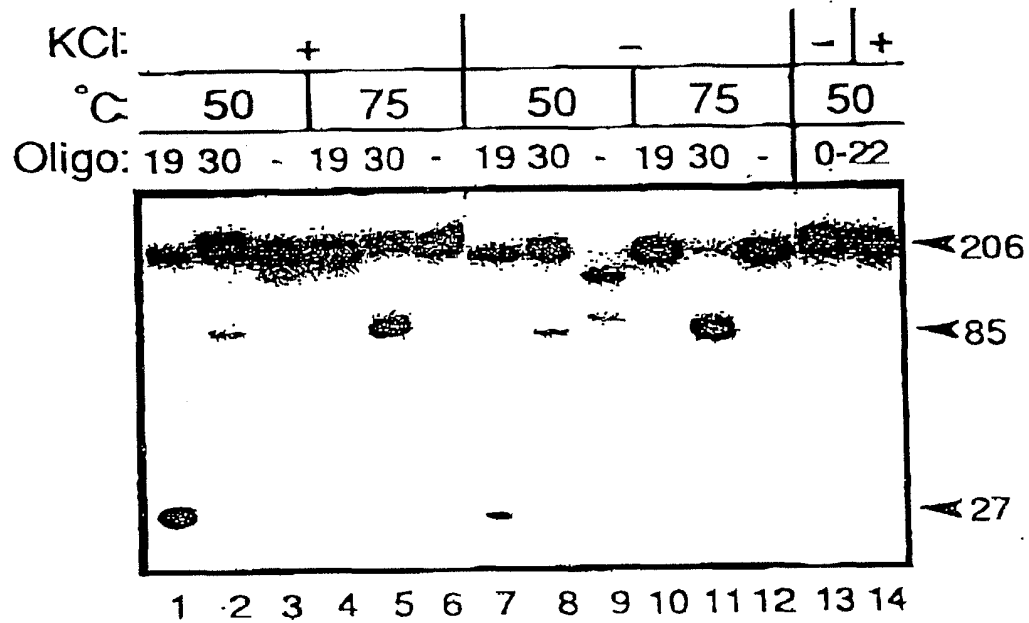


FIGURE 11B

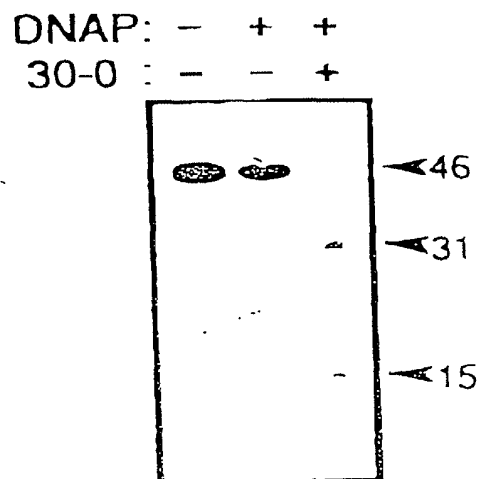


FIGURE 12B

21

[REDACTED]

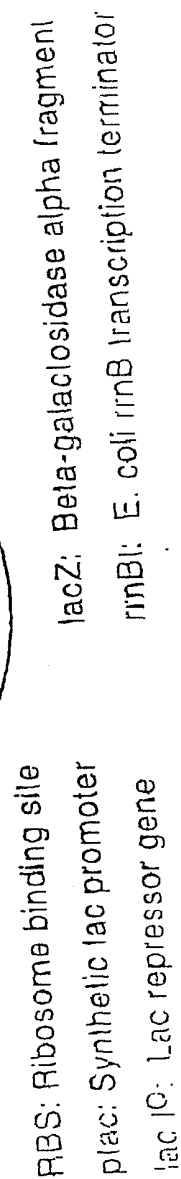
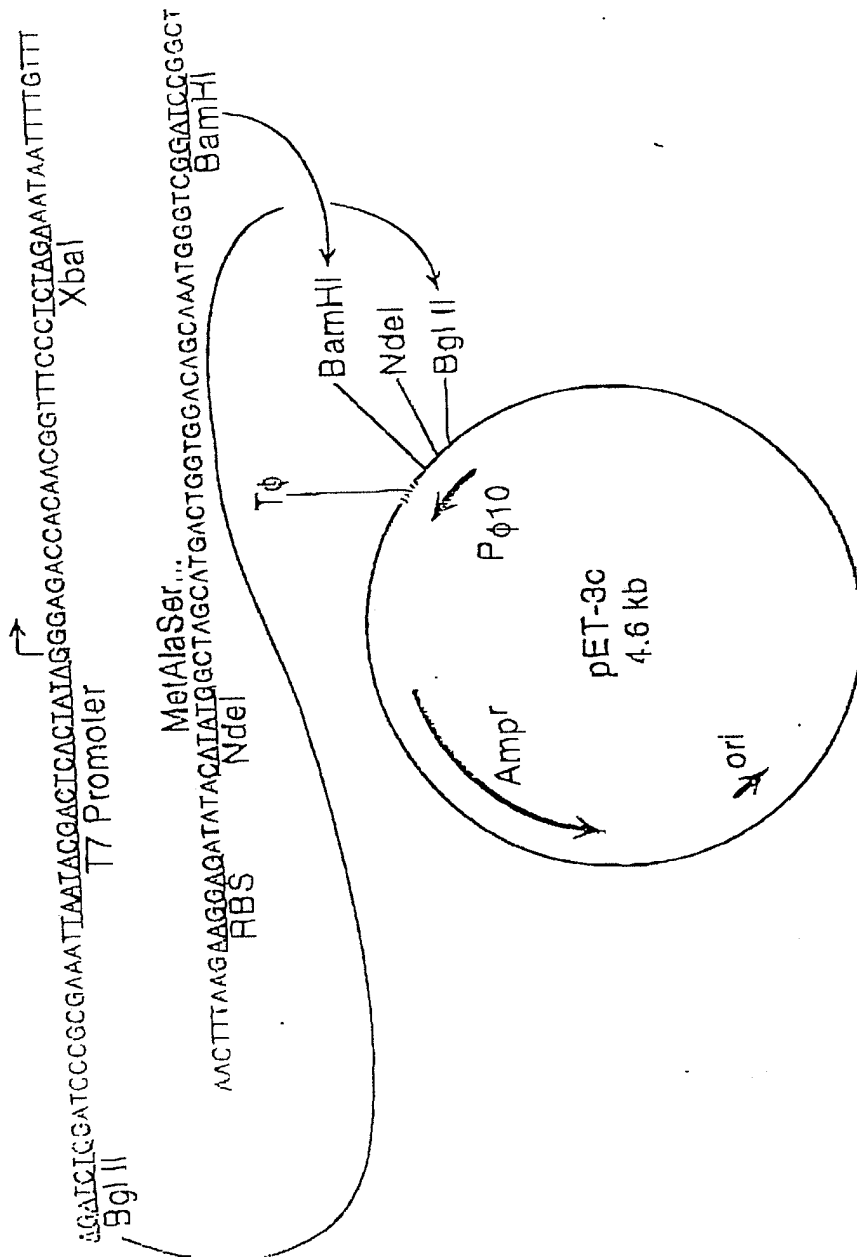


FIGURE 14

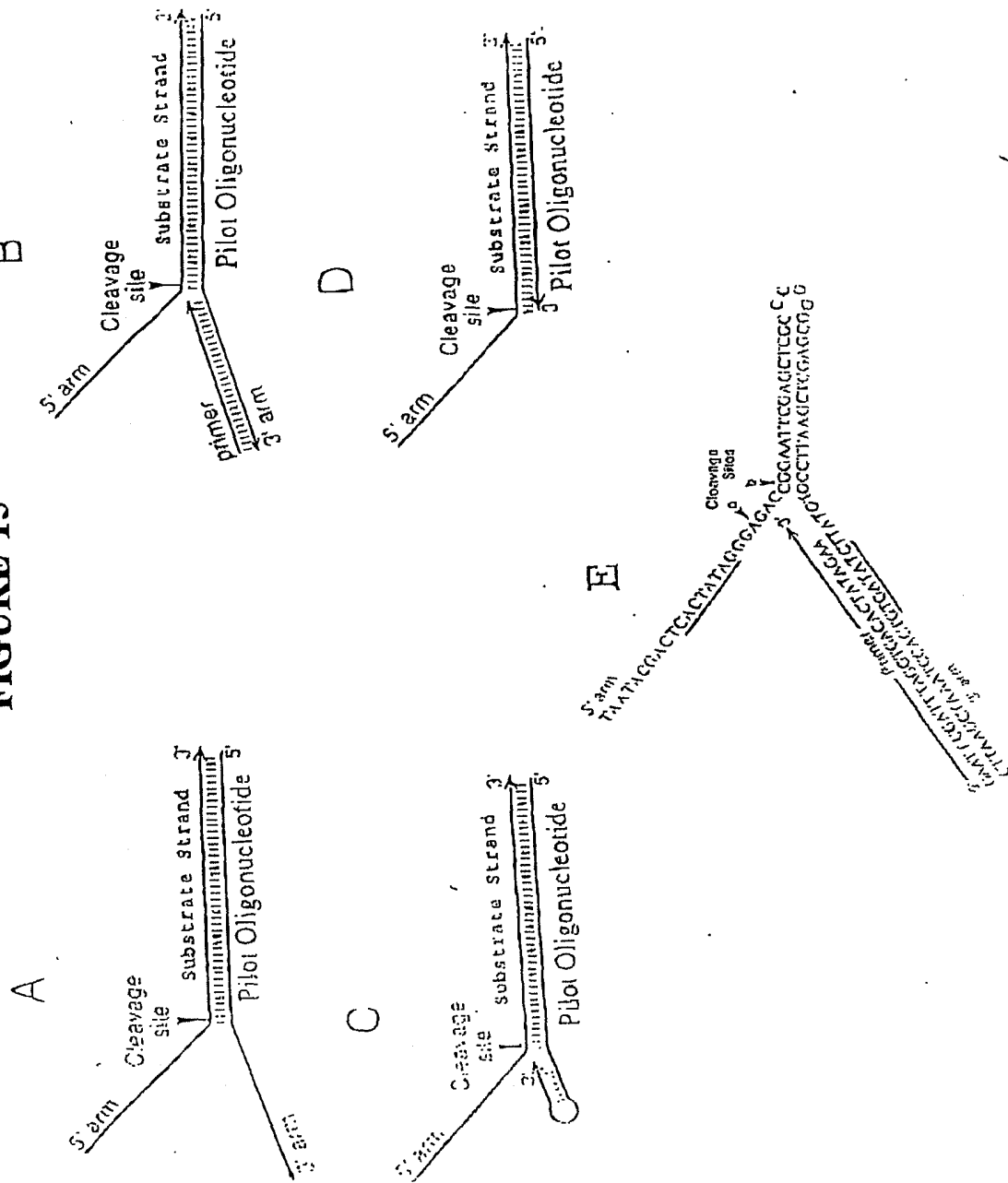


RBS: Ribosome binding site

P_{φ10}: Baculovirus P10 promoter

T_φ: T7 terminator

FIGURE 15



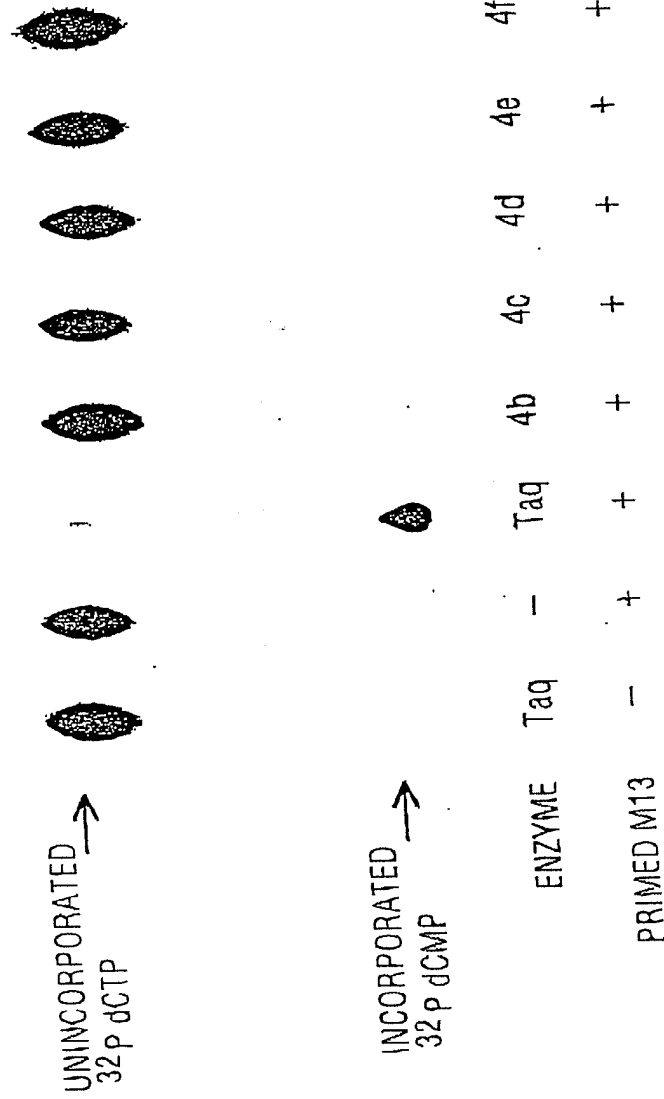


FIGURE 17

1103 5525 3403

42

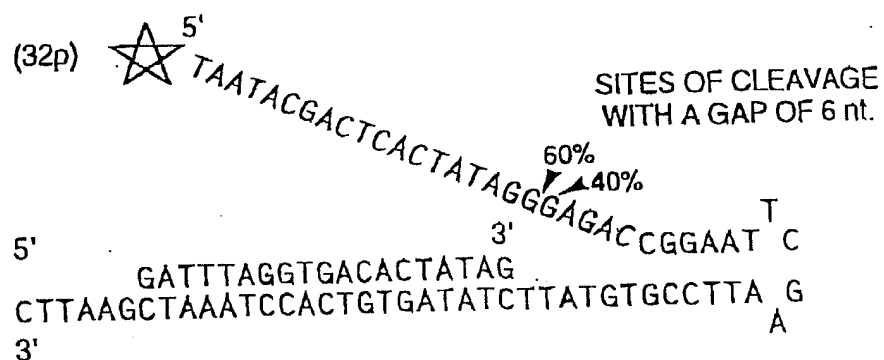


FIGURE 18A

	"4d"				"4b" 2 PT. MUTATION SMALL ACTIVITY		UNMODIFIED DNAP Taq		dNTP
	1	2	3	4	5	6	7	8	
	-	-	-	-	-	-	-	-	+
	+	+	+	+	+	+	+	+	+

84 NUC. —

HAIRPIN TEST MODULE

CONVERSION TO DOUBLE STRANDED (COMPLETE EXTENSION OF PRIMER)

MULTIPLE BANDS CAUSED BY POLYMERIZATION

DESIRED PRODUCT 21 NUC.

SOME ABERRANT CLEAVAGE WITH "4b" BECAUSE OF RESIDUAL POLYMERASE ACTIVITY.

FIGURE 18B

PsII BspMI
 Sph I
 Hinc III
 PstI
 PstI 30-0
 SP6
 228
 206

100033297 140201

I II III IV V VI
1 1 2 3 1 2 3 1 1 2 3 1 1 2 3 1 2 3
1 1 2 3 1 2 3 1 1 2 3 1 1 2 3 1 2 3

— 206

— 85

206 —

85 —

FIGURE 20B

31

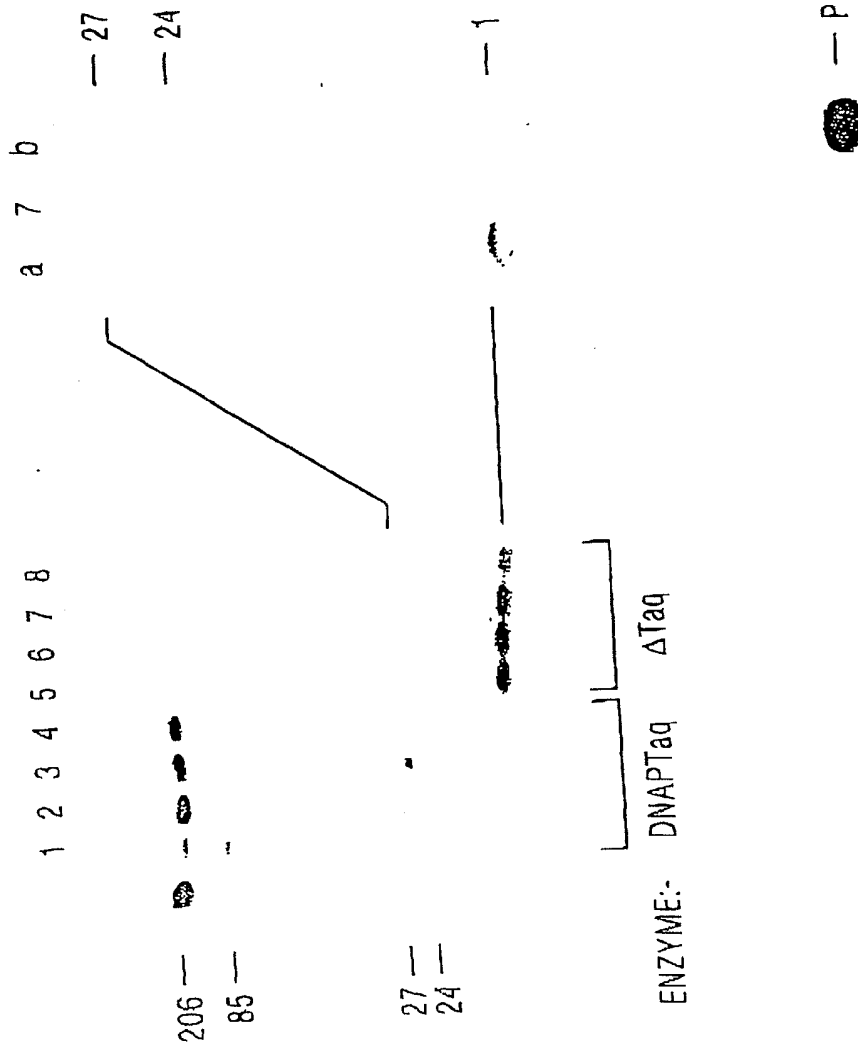
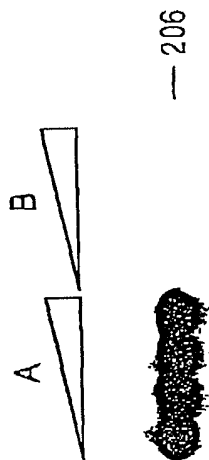


FIGURE 21B

FIGURE 21A

FIGURE 22A



— 206



* = 32p

FIGURE 22B

[Handwritten musical notation]



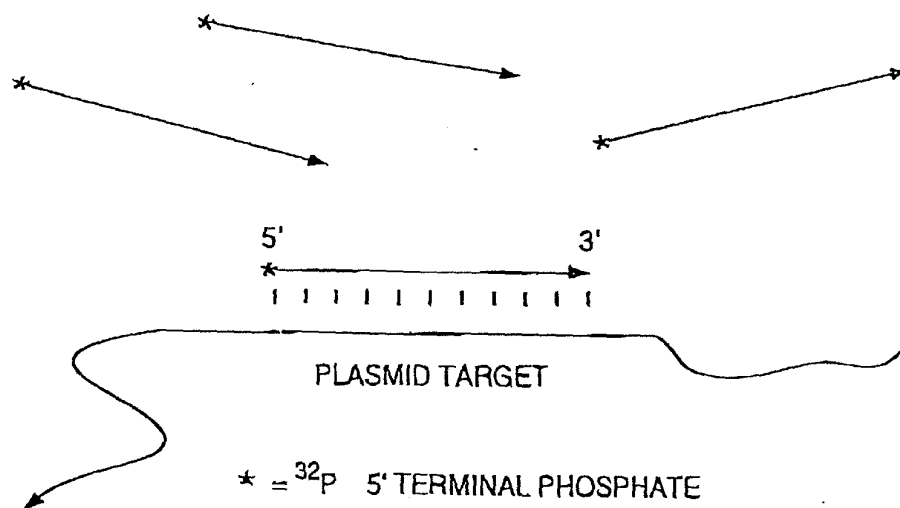


FIGURE 24A

35

FIGURE 25

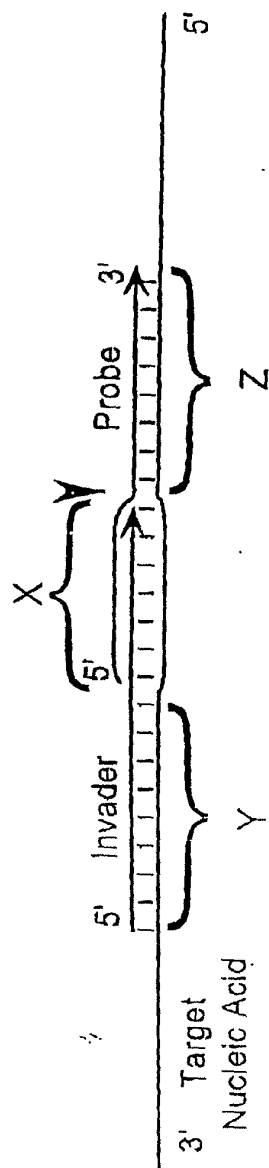
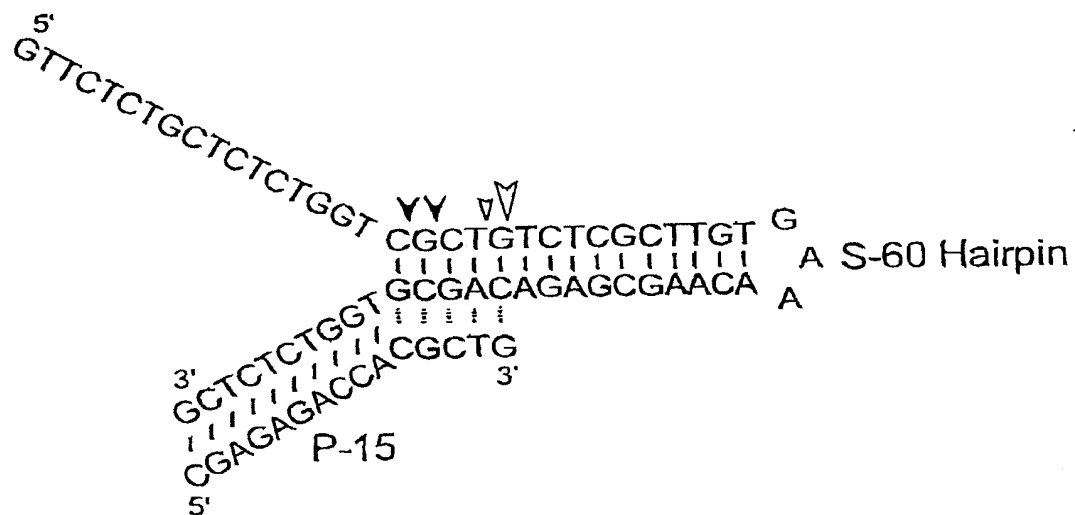


FIGURE 26



39

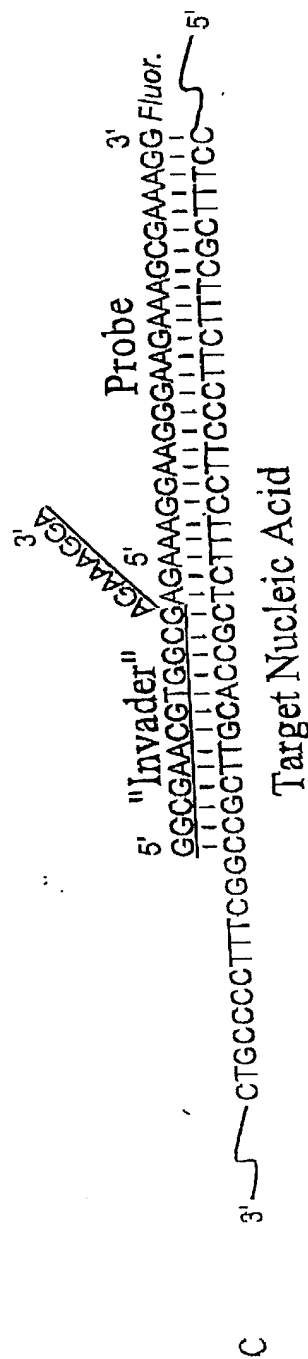
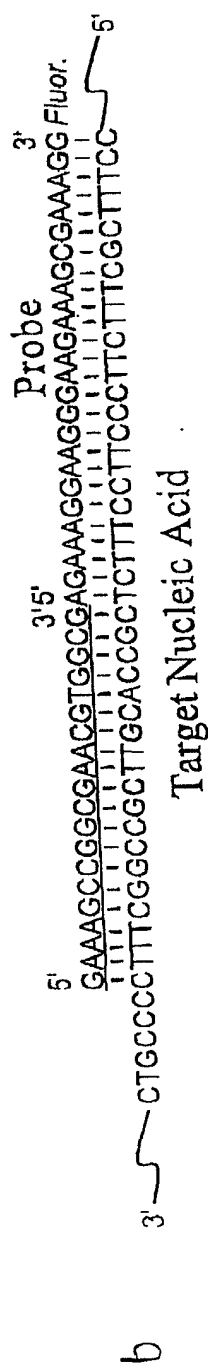
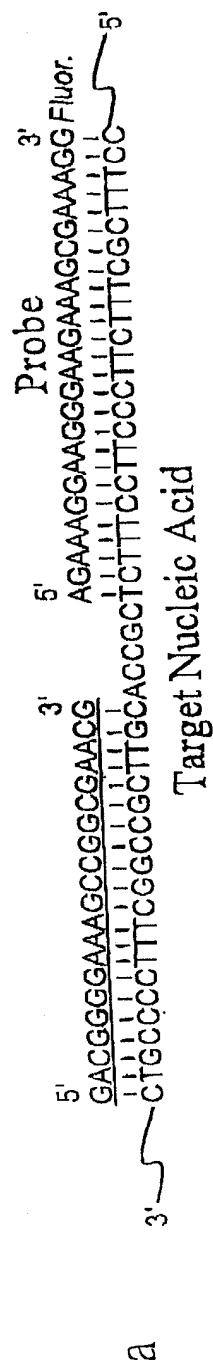
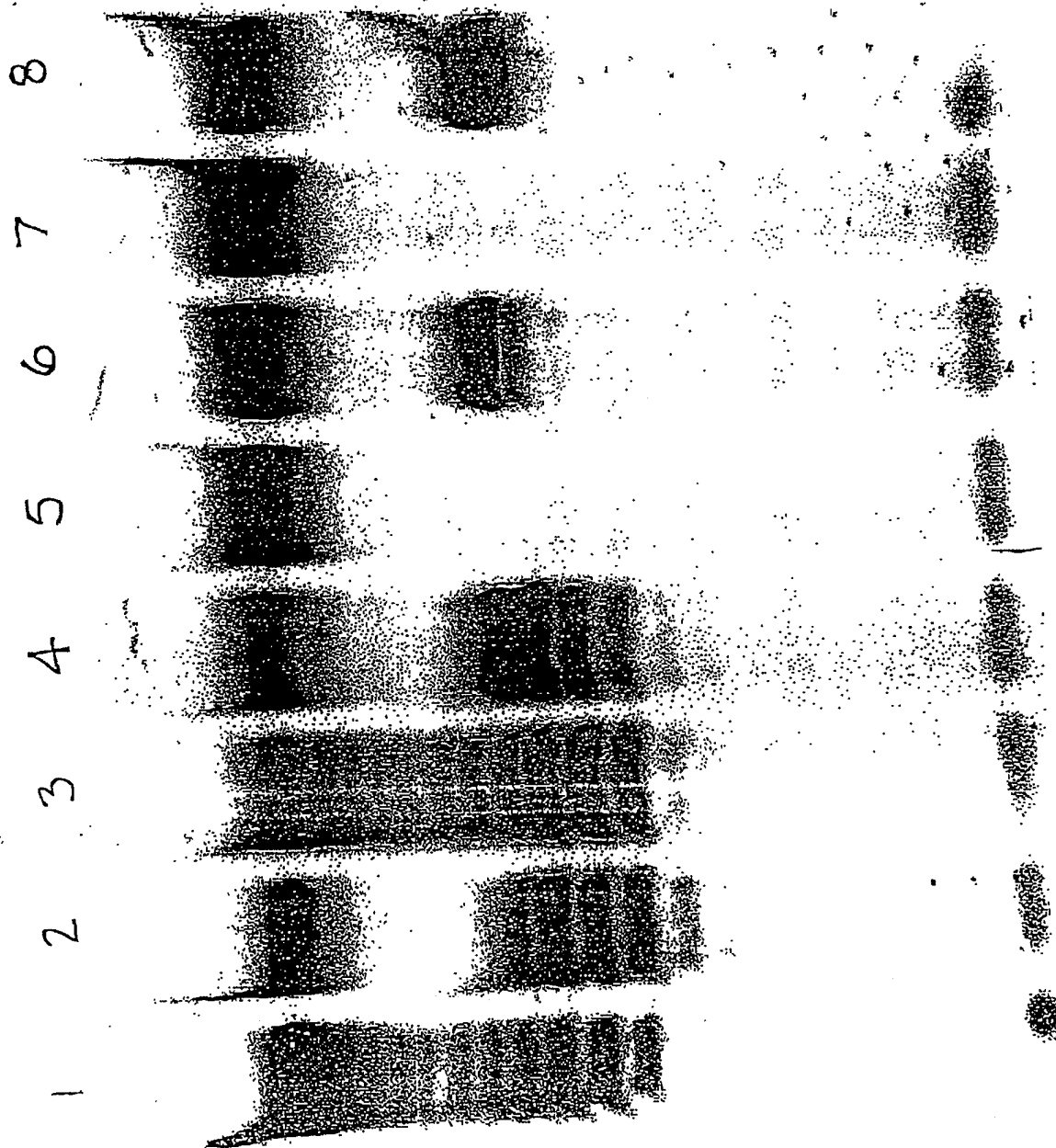


FIGURE 29



26

FIGURE 32

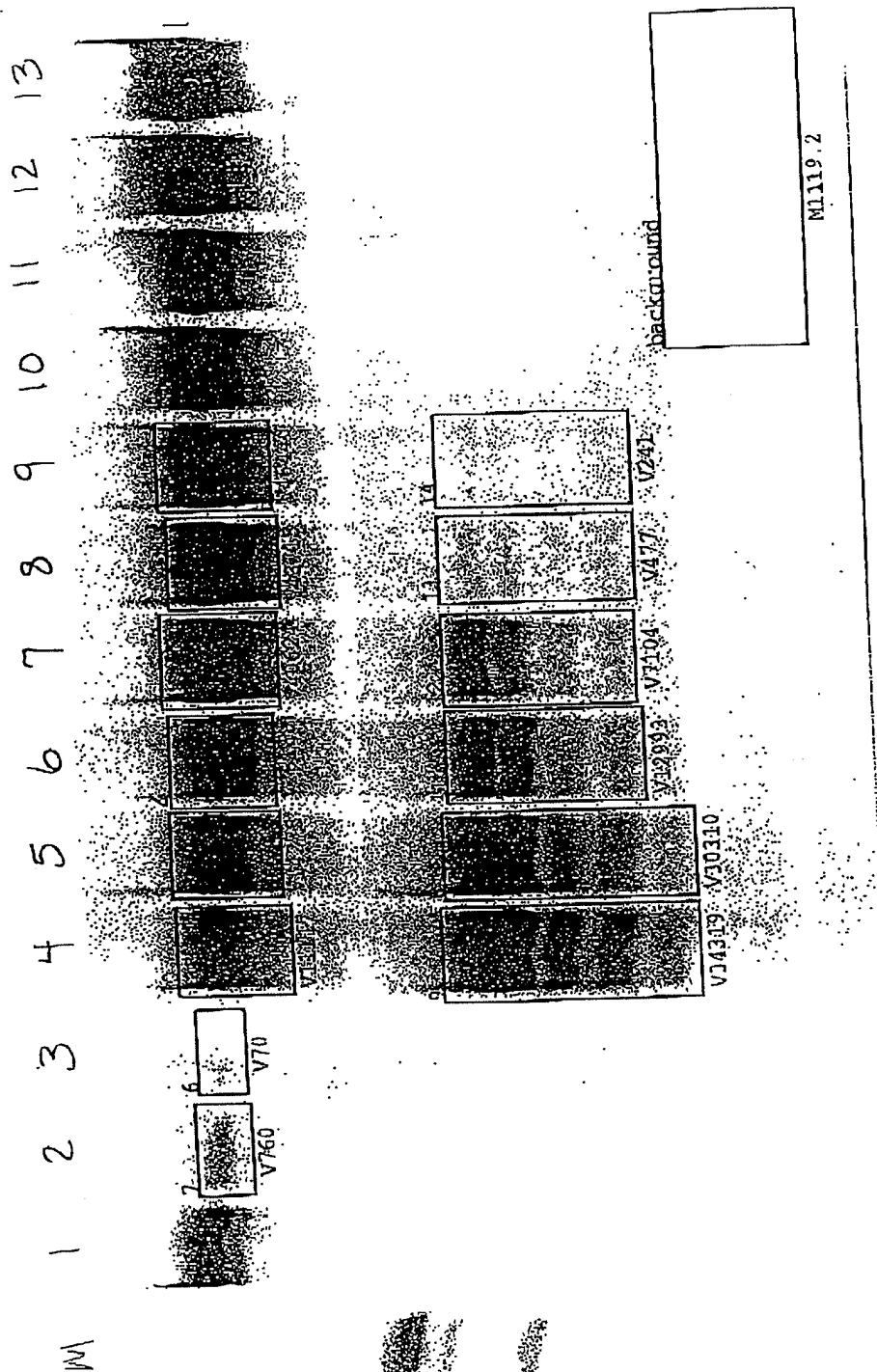
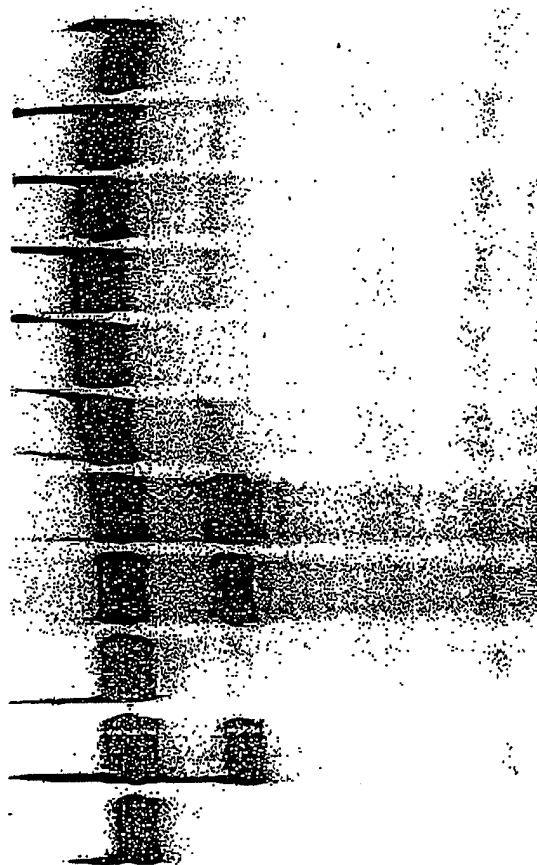


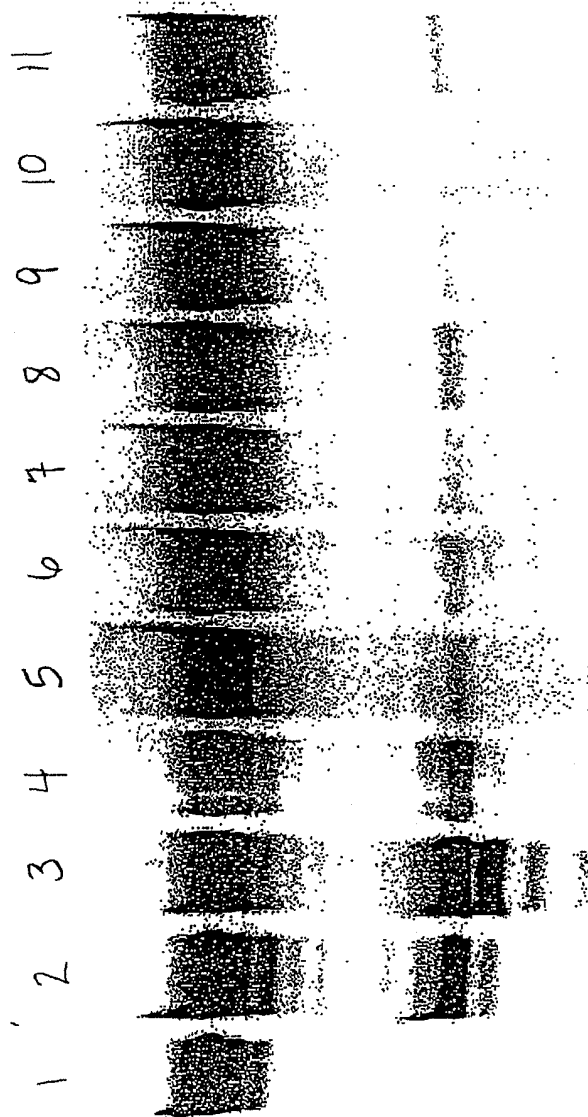
FIGURE 33

1 2 3 4 5 6 7 8 9 10 11



A A

FIGURE 34



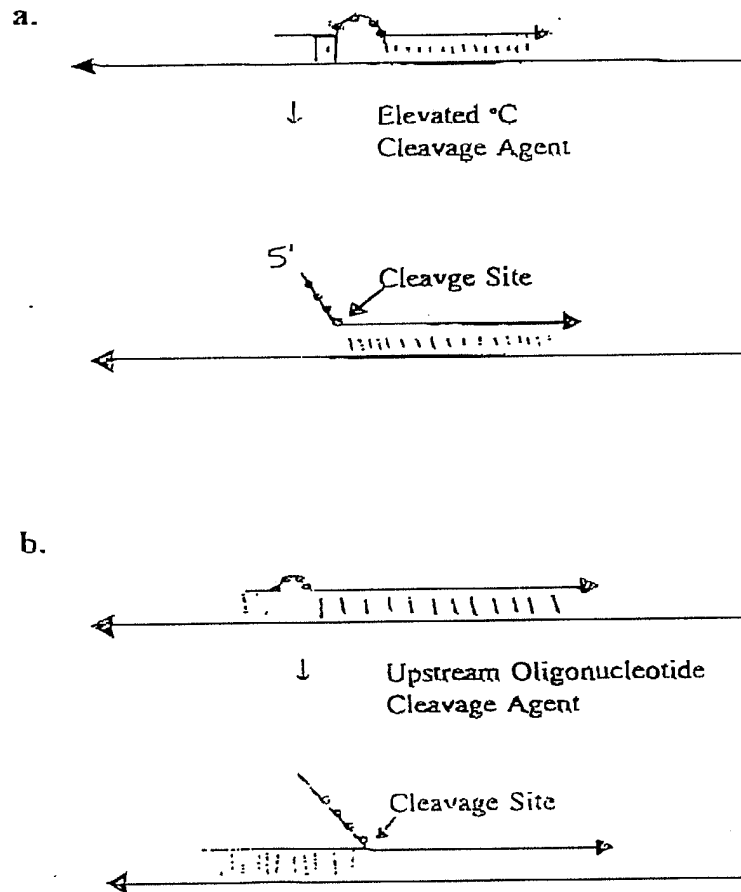


FIGURE 36

Invasive Cleavage Directing Oligo

Cleavage Site

Probe Oligomer

[illegible]

FIGURE 37

FIGURE 38

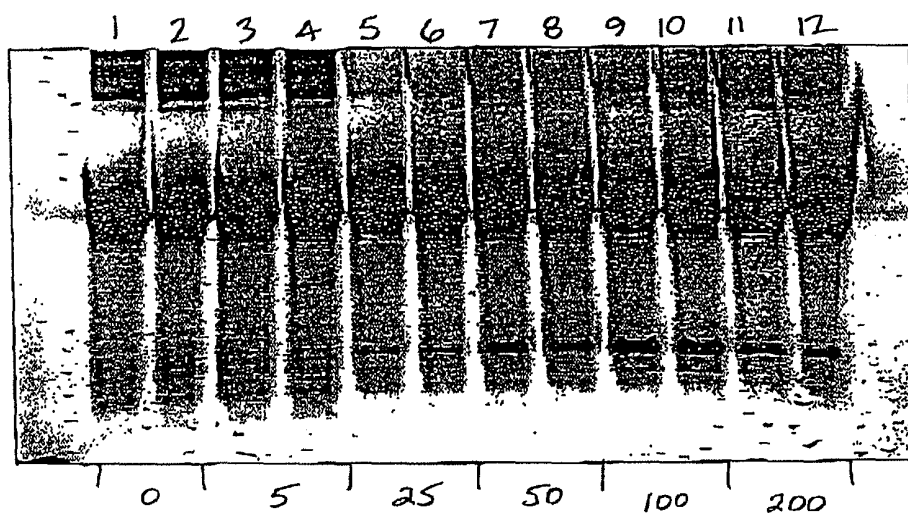


FIGURE 39

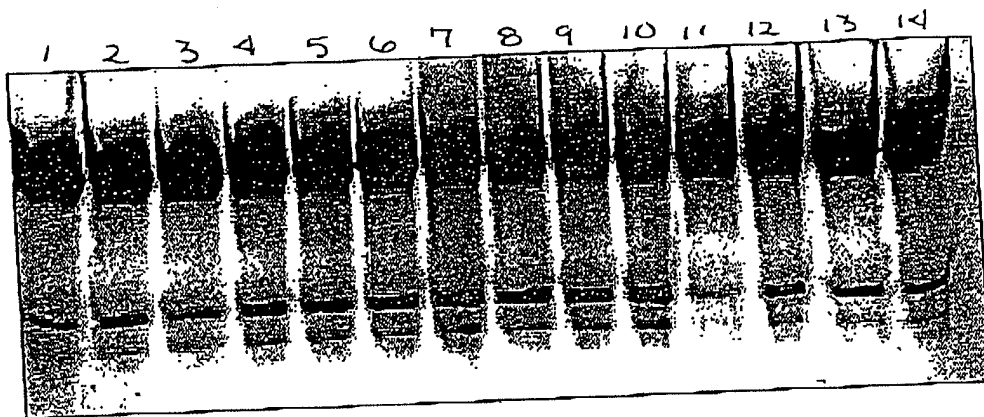


FIGURE 40

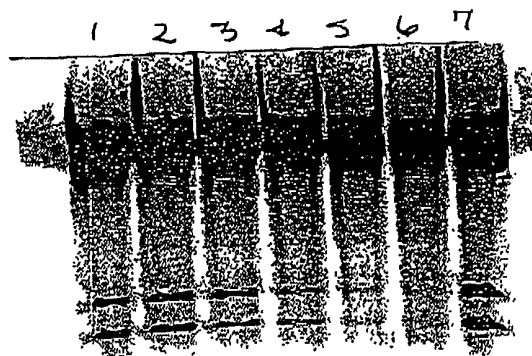


FIGURE 41

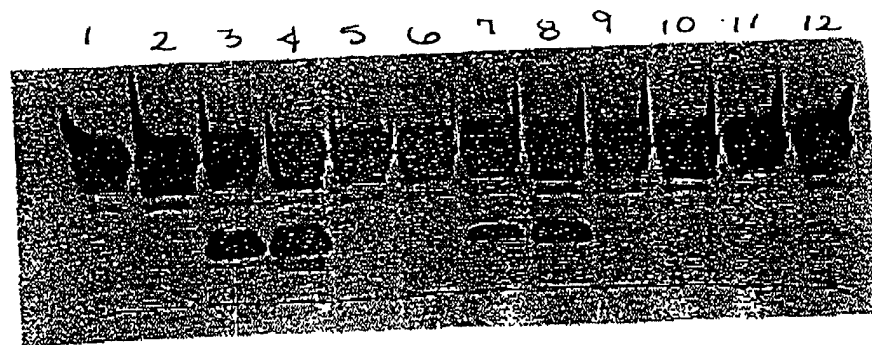
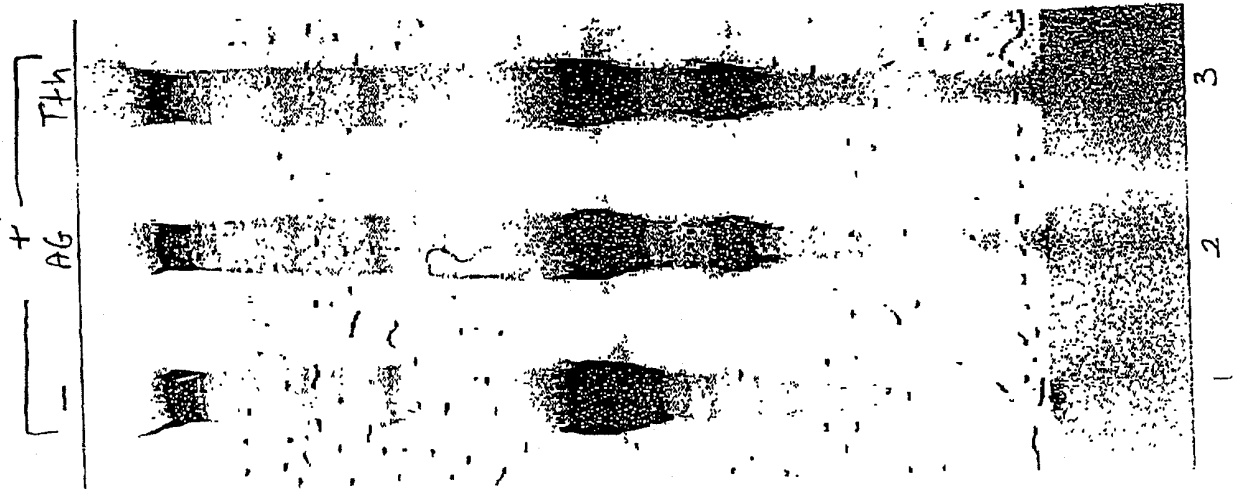


FIGURE 42B



FIGURE 42A



target RNA

uncleaved
probe

cleaved
probe

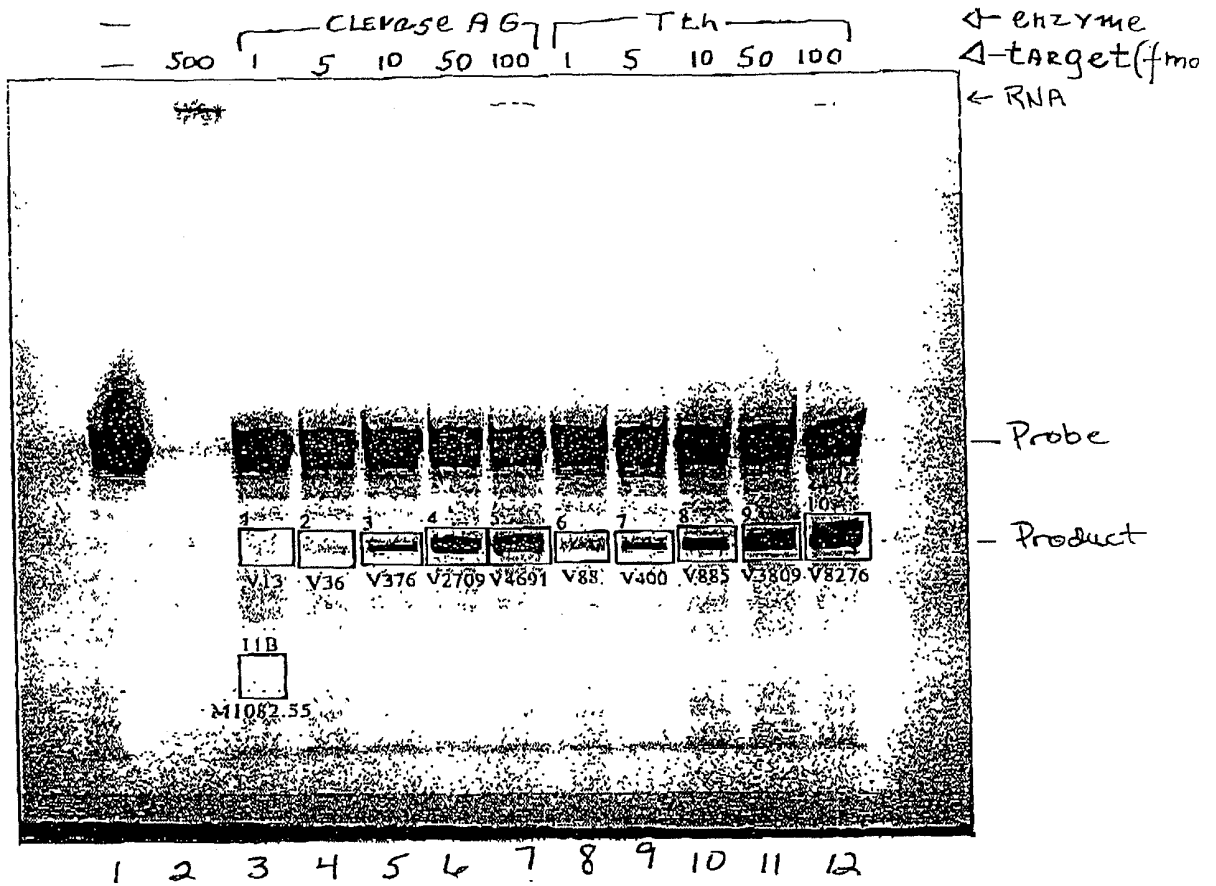


FIGURE 43

55

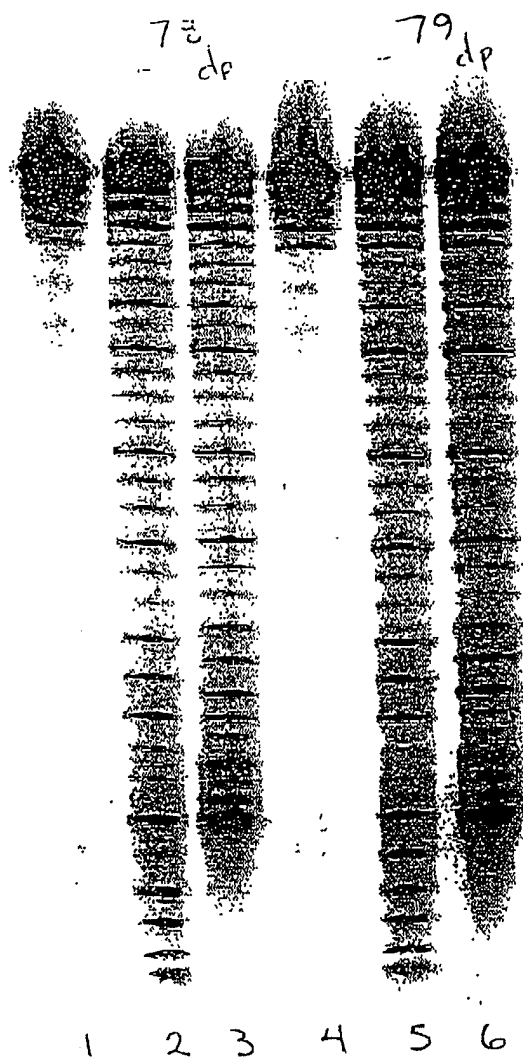
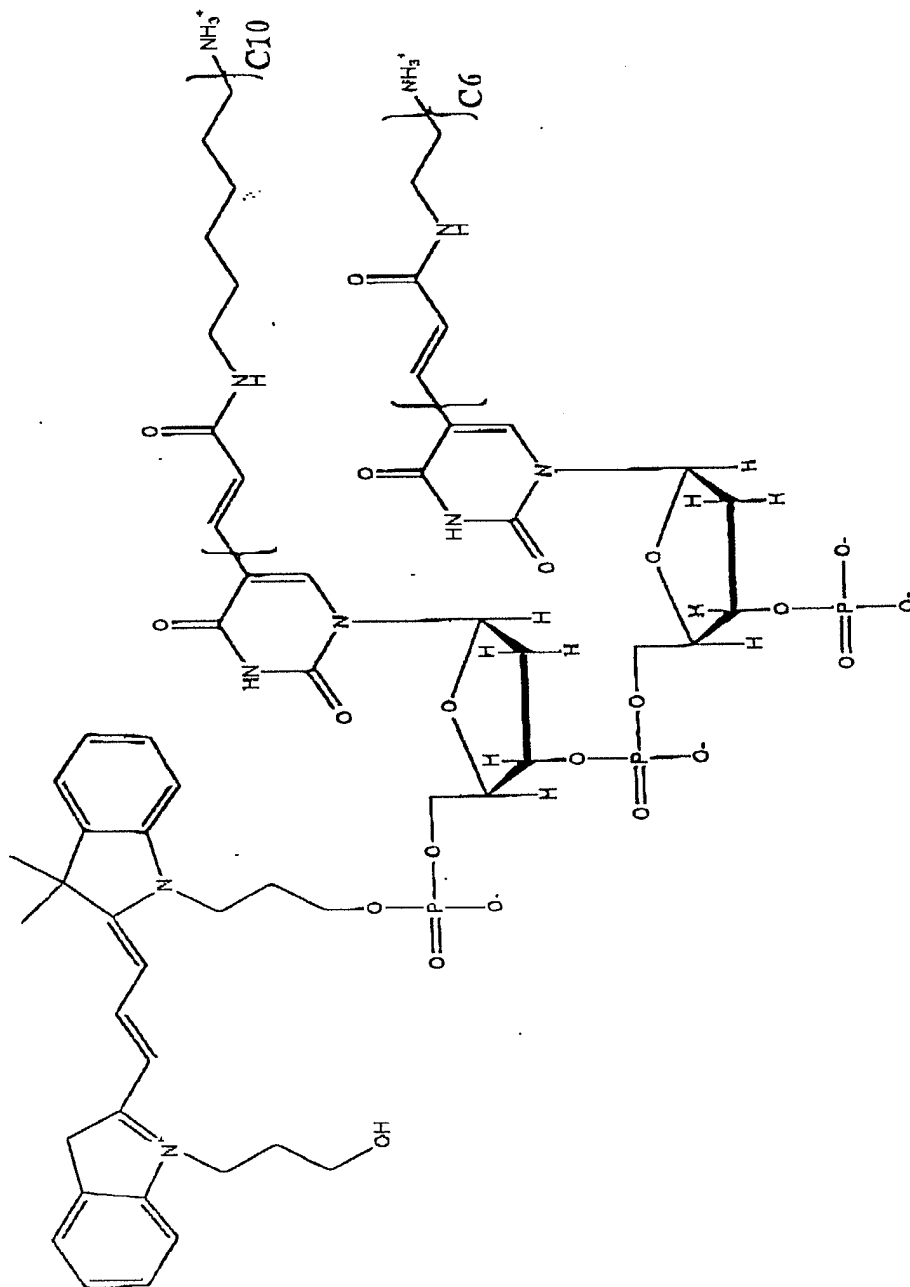


FIGURE 44

FIGURE 45

70 (C10 aminoT's)

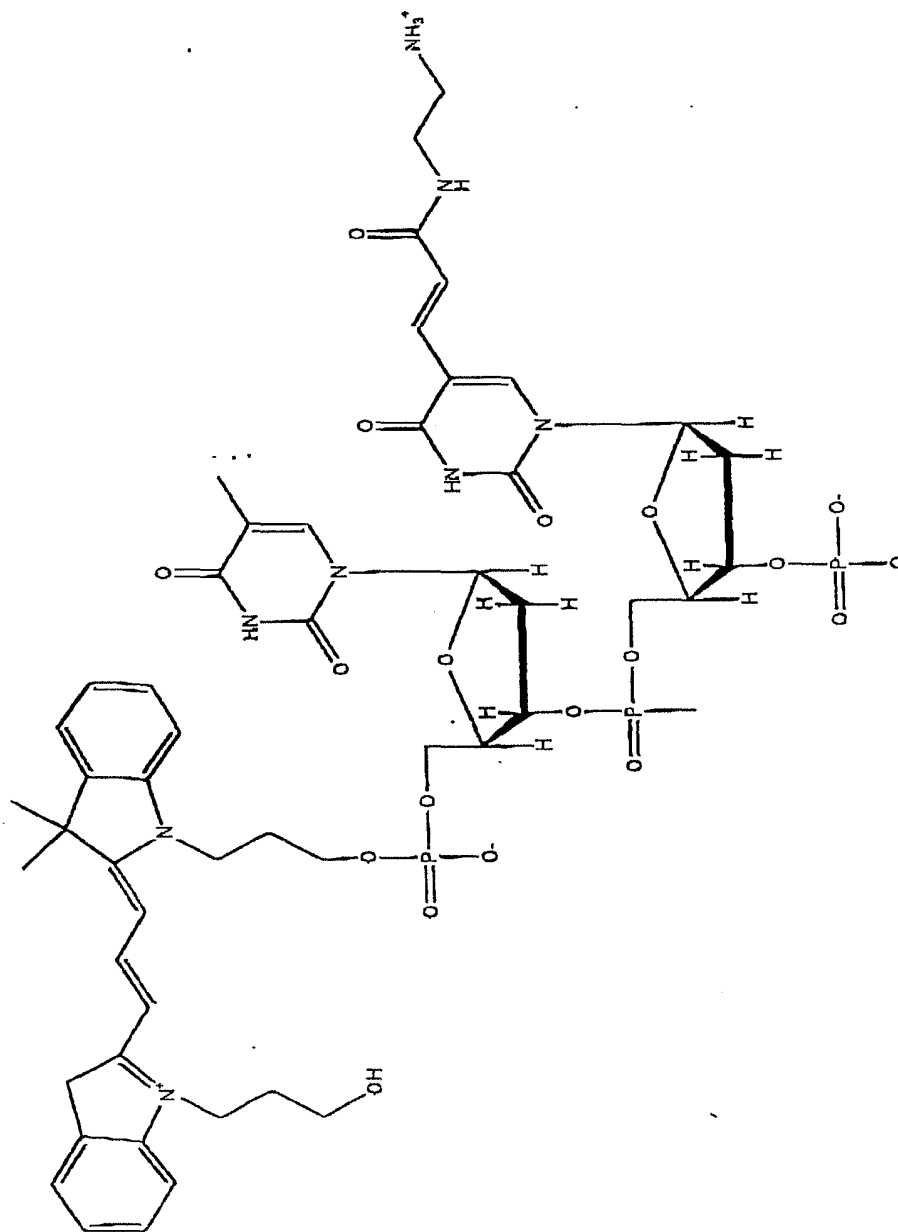
74 (C6 amino T's)



57

FIGURE 46

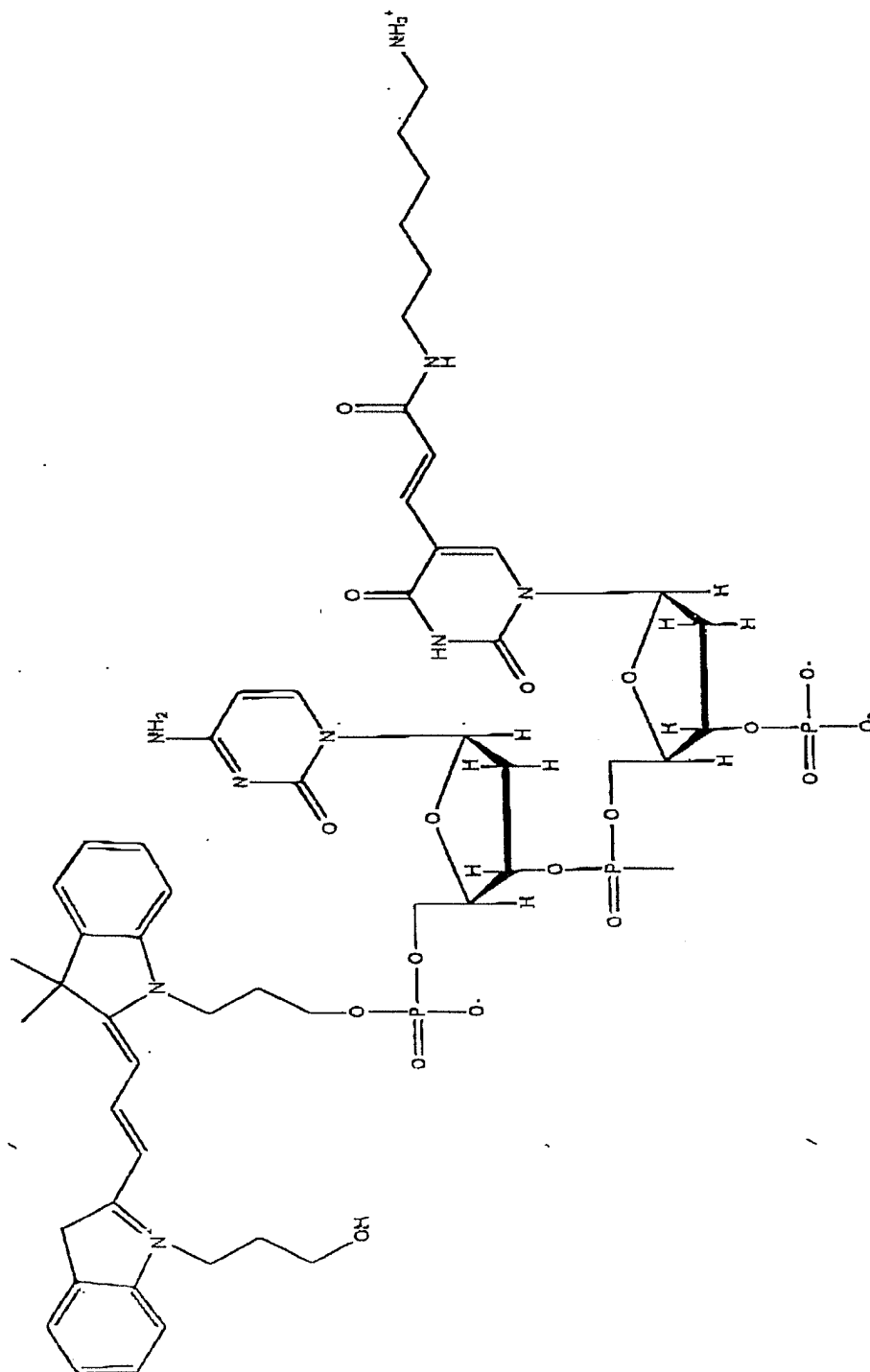
75



58

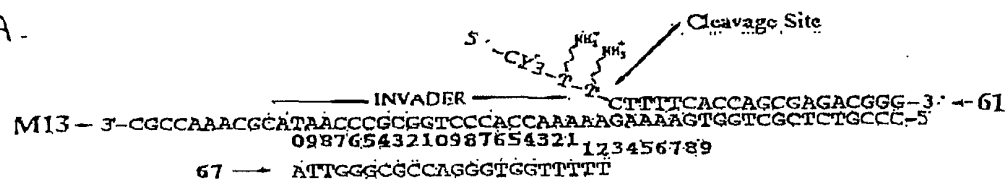
FIGURE 47

76



60

A.



B.

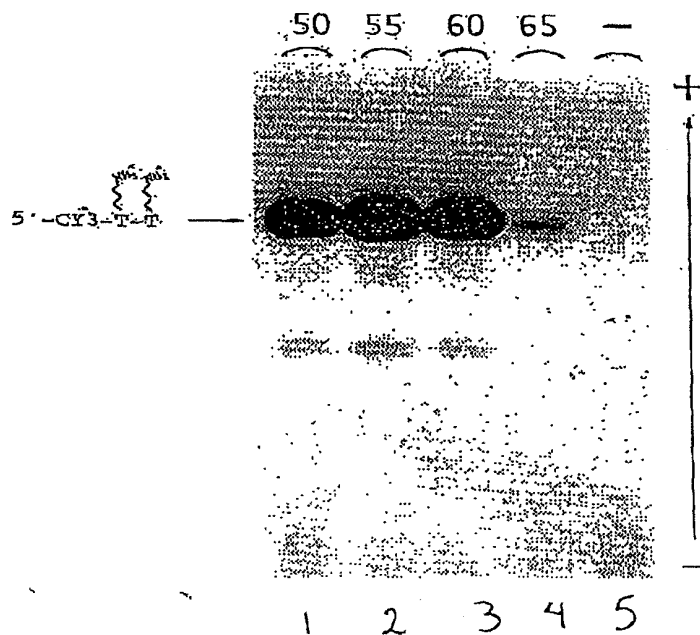


FIGURE 49

6

ALL INFORMATION CONTAINED HEREIN IS UNCLASSIFIED



62

FIGURE 51

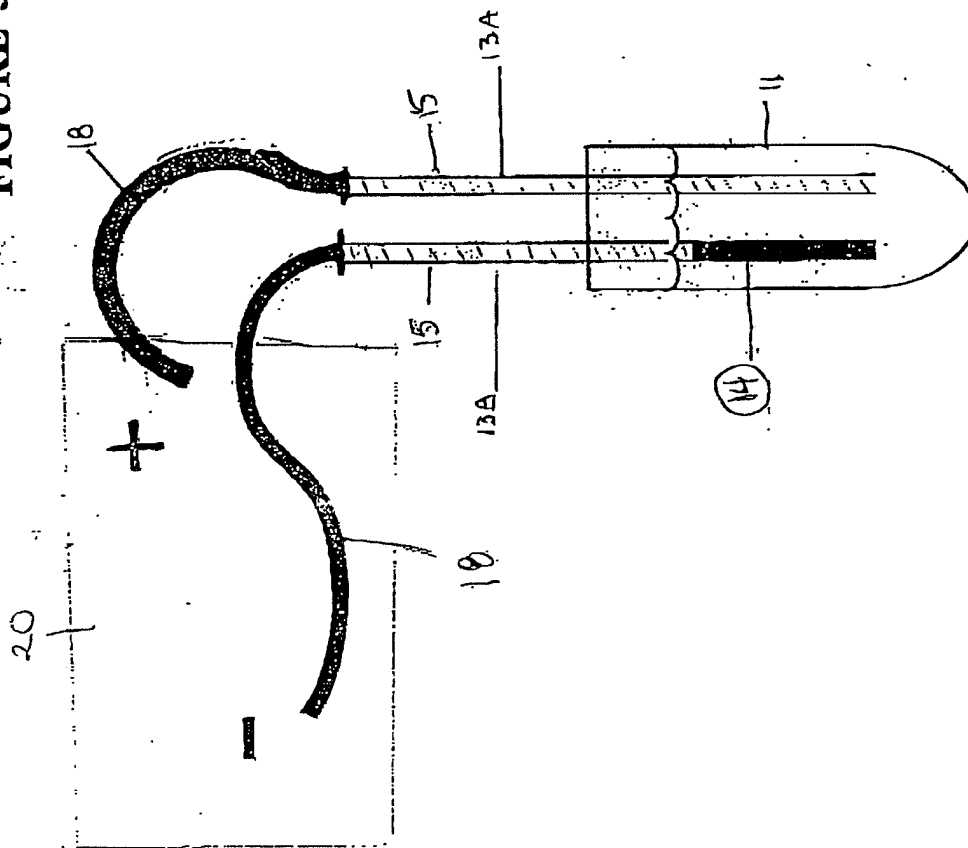


FIGURE 52

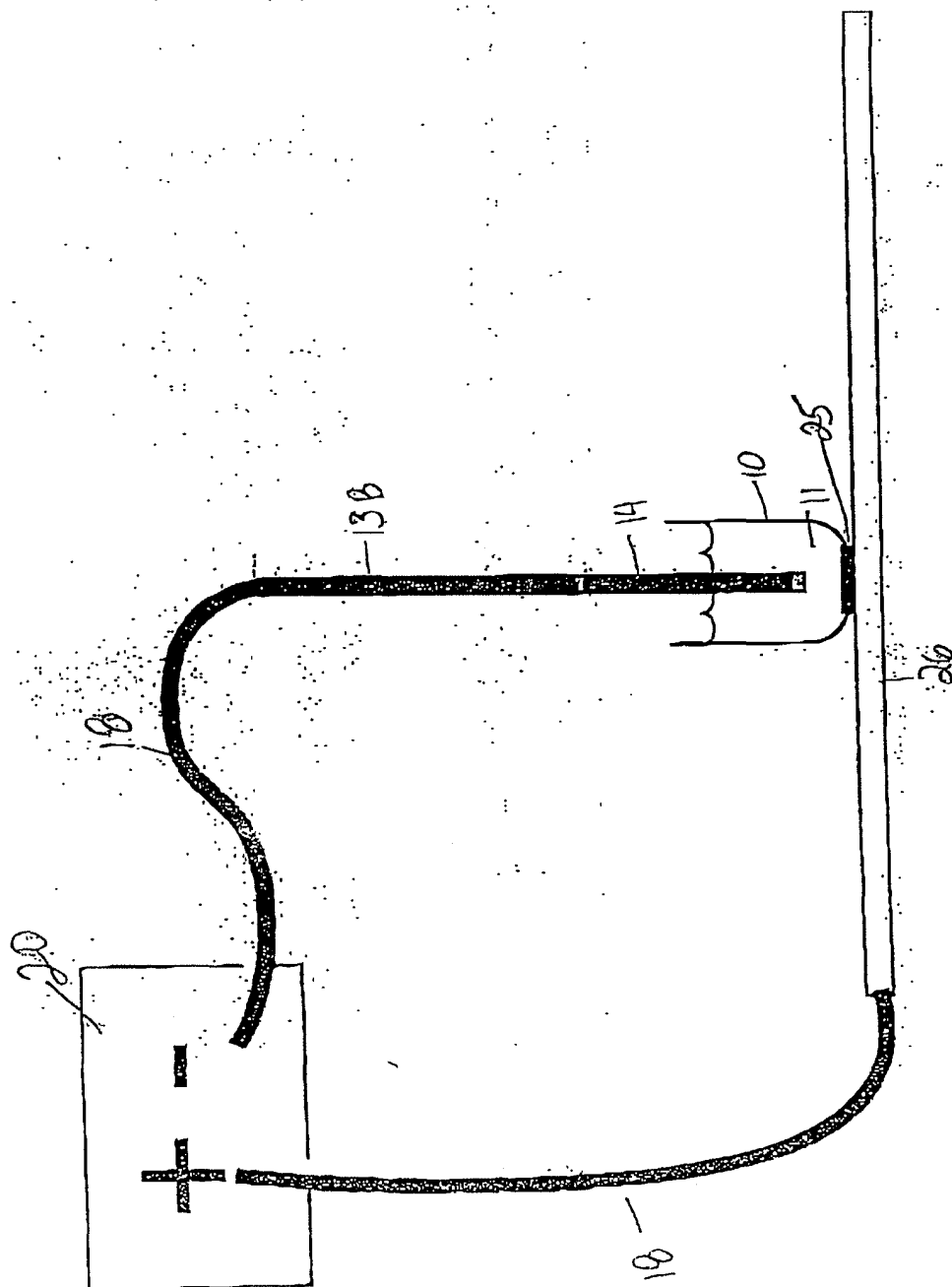
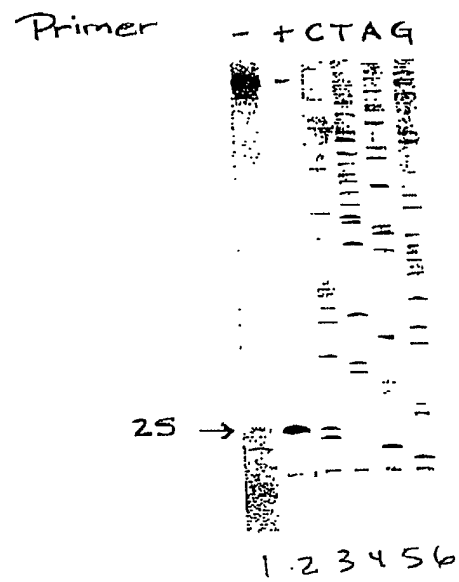


FIGURE 53



5' AGAAAGGAAGGGAAGAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

AGAAAGGA

a

5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

5' CAG AAGGAAGGGAAGAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

CAGAAGGA

b

5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

5' CAGGG GGAAGGGAAGAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

CAGGGGGA

c

5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

5' CAGGGTAC AGGGAAGAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

CAGGGTAC

d

5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

FIGURE 54

FIGURE 55

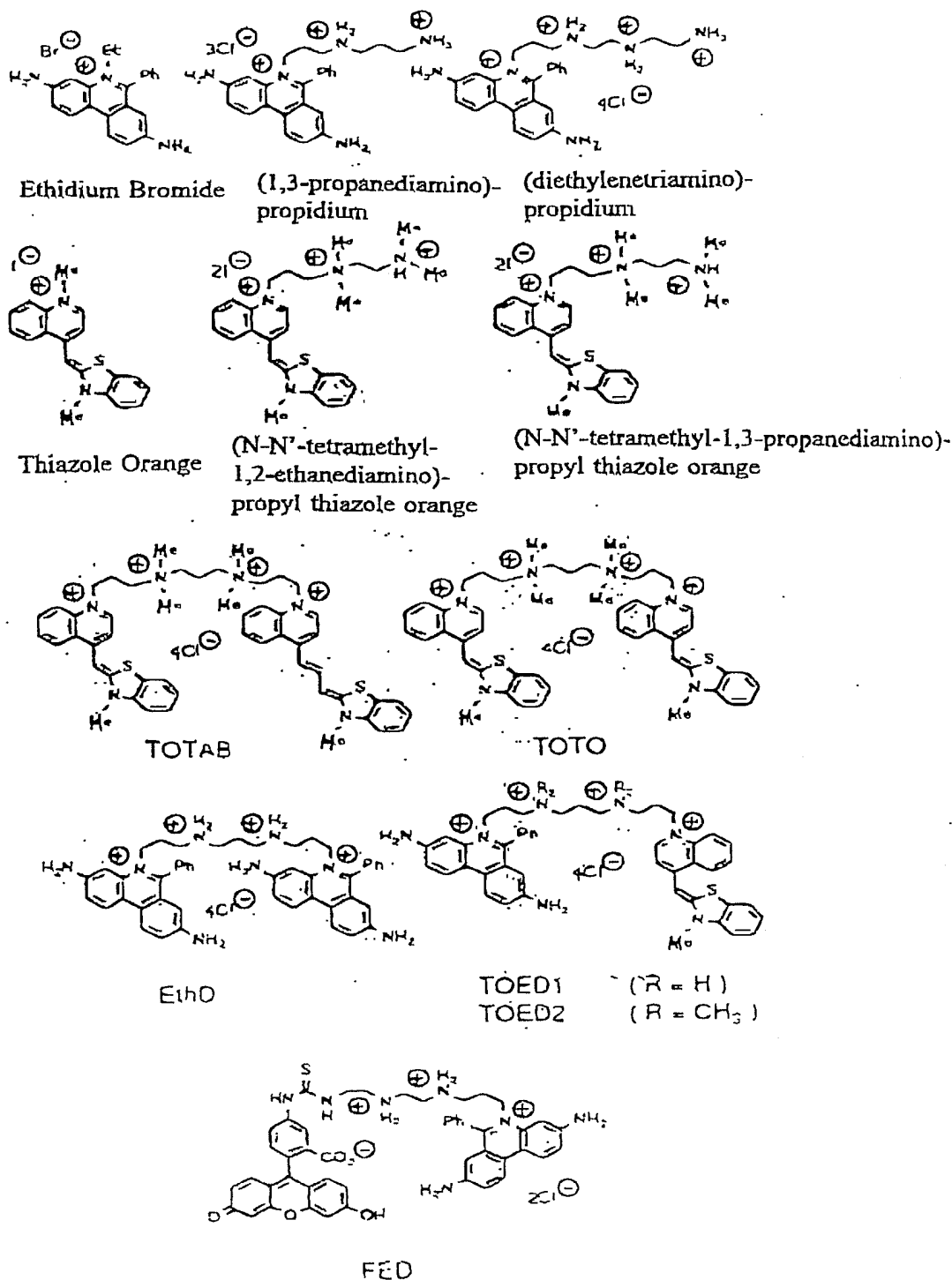


FIGURE 30

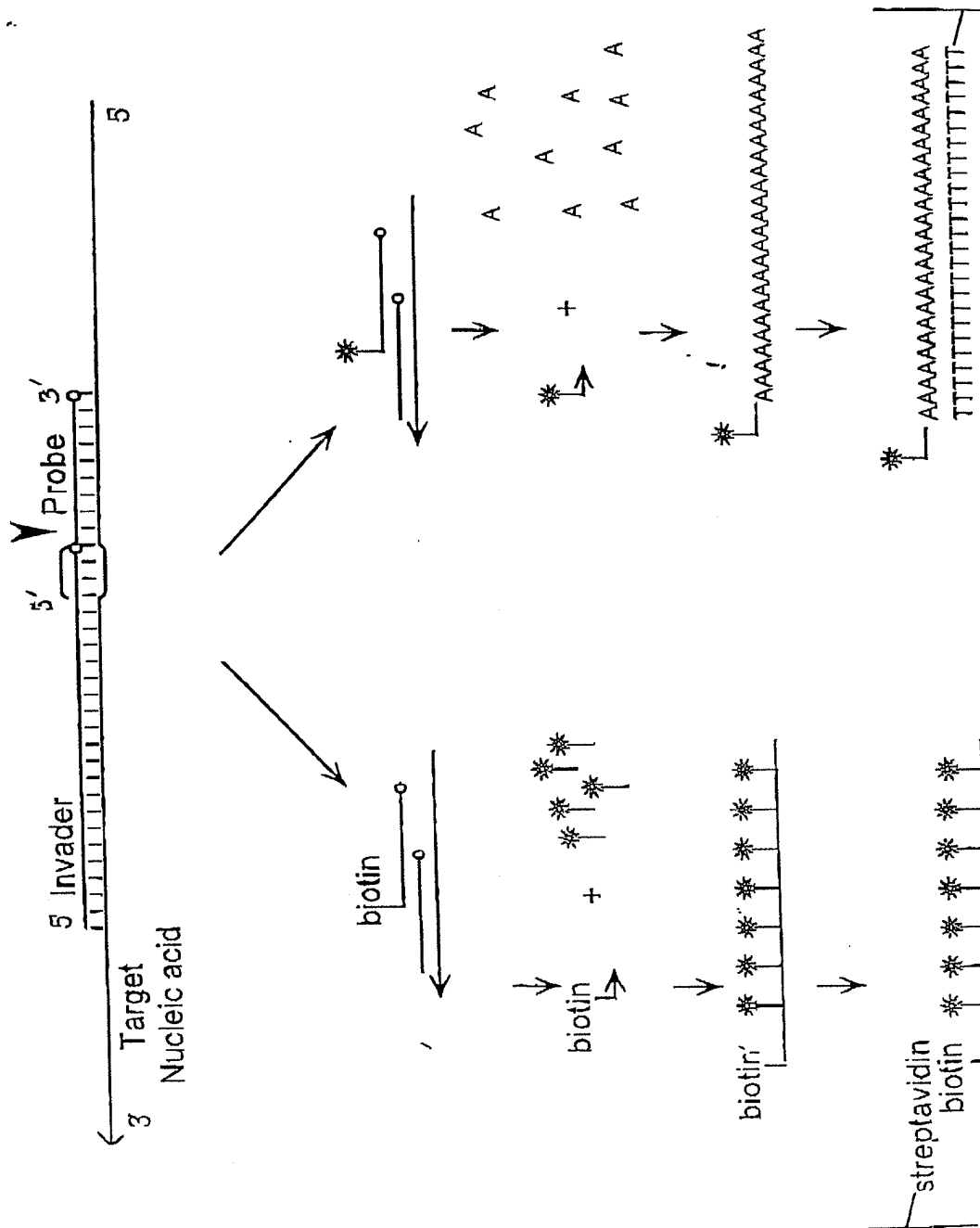
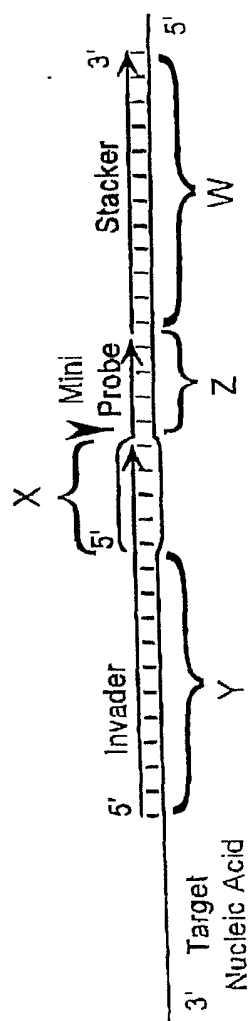


FIGURE 57



11-11-68

	10	20	30	40	50	60	70
-----GDFIPK----	NISFEDLKGGKVAIDGMNALYQFLTSIRLROGSPLNRKGEITSAYNGVFY	MJAFENI.PRO					
-----ICEIPR--KEIELENLYGKKIAIDALNAIYOFLSTIRQKDGTPLMSDKGRITSHLSGLFY	PFUFENI.PRO						
-----GLAKLIADVAPSAIRENDIKSYFGKRKVAIDASMSIYOFLIAVRQ-GGOVLONEEGETTSHLMGMFY	HUMFENI.PRO						
-----GLAKLIADVAPSAIRENDIKSYFGKRKVAIDASMSIYOFLIAVRQ-GGOVLONEEGETTSLMGMFY	MUSFENI.PRO						
-----GLAKLIADVAPSAIRENDIKSFFGKRKVAIDASMSLYQFLIAVROODGGOLTNEAGETTSHLMGMFY	YST5IO.PRO						
-----GLNLISEHVPSAIRKSOKSFFGKRKVAIDASMSLYQFLIAVROODGGOLTVNAAGETTSHLMGMFY	YSTRAD2.PRO						
-----HSHFWDIAG----PTARPVRLSELEDKRMMAVDASIIWYQFLKAVRODEGNVKN-----SHITGFFR	SPORAD13.PRO						
-----SGLWNILE----PVKRPVKLETLVNKRLAIDASIIWYQFLKAVRODEGNOLKS-----SHUVGFRR	HUMXPG.PRO						
-----DGLWKLE----CSGROVSPEALEGKI LAVDISIWLNOALKGVDRDHGNSIEN-----PHLLTLFH	MUSXPG.PRO						
-----DGLWKLE----CSGHRVSPEALEGKVLAVIDISIWLNOALKGVDRDSHGNIEN-----AHLLTLFH	XENXPG.PRO						
-----DGLWKLE----CSGRP INPGLTEGKI LAVDISIWLNOAVKGARDOROGNAION-----AHLLTLFH	CELRAO2.PRO						
-----DGLWKLE----CSGRP INPGLTEGKI LAVDISIWLNOAVKGARDOROGNAION-----PNSYLVTFT							
-----GMEWANHVV----RKVPNETMROKTLSDIGHIWLYESLKGCEAHHOOT-----PNSYLVTFT							
	20	90	100	110	120	130	140
-----HLLENDIPTIIVFDGEPKPKKEKTRKVRREMKEKAELKMKEAIKK-----EDFEEAAKYAKRVSYLTTP	MJAFENI.PRO						
-----HLLMEAGIKPYVVFDCGEPPEFKKKKELEKREAREAEAEKWRREALK-----GEJEERARYAQORATRVNE	PFUFENI.PRO						
-----HLLMEAGIKPYVVFDCGEPPEFKKKKELEKREAREAEAEKWRREALK-----GAEOVEKFTRLVKVTK	HUMFENI.PRO						
-----HLLMEAGIKPYVVFDCGEPPEFKKKKELEKREAREAEAEKWRREALK-----GMEEEVEKFTRLVKVTK	MUSFENI.PRO						
-----HLLMEAGIKPYVVFDCGEPPEFKKKKELEKREAREAEAEKWRREALK-----TTELEKMKOERRLVKVS	YST5IO.PRO						
-----HLLMEAGIKPYVVFDCGEPPEFKKKKELEKREAREAEAEKWRREALK-----TTELEKMKOERRLVKVS	YSTRAD2.PRO						
-----HLLMEAGIKPYVVFDCGEPPEFKKKKELEKREAREAEAEKWRREALK-----TTELEKMKOERRLVKVS	SPORAD13.PRO						
-----HLLMEAGIKPYVVFDCGEPPEFKKKKELEKREAREAEAEKWRREALK-----TTELEKMKOERRLVKVS	HUMXPG.PRO						
-----HLLMEAGIKPYVVFDCGEPPEFKKKKELEKREAREAEAEKWRREALK-----TTELEKMKOERRLVKVS	MUSXPG.PRO						
-----HLLMEAGIKPYVVFDCGEPPEFKKKKELEKREAREAEAEKWRREALK-----TTELEKMKOERRLVKVS	XENXPG.PRO						
-----HLLMEAGIKPYVVFDCGEPPEFKKKKELEKREAREAEAEKWRREALK-----TTELEKMKOERRLVKVS	CELRAO2.PRO						

FIGURE 59B

	150	160	170	180	190	200	210
25	WENCKYLLSLMGIPYVEAPSEGEAQASYMAKKGDVWAVVSQDYDALLYGAPRVVRNLITTKEM----						MJAFEN1.PRO
30	EDAKYLLLELMGPIVOAPSEGEAQAAAYMAAKGSVYASQDYDLSLLFGAPRLVRNLITGKRKLPGK						PFUFEN1.PRO
35	HNDECKHLLSLMGIPYLDAPSEAEASCAALVKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPIQ						HUMFEN1.PRO
40	HNDECKHLLSLMGIPYLDAPSEAEASCAALAKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPIQ						MUSFEN1.PRO
45	VEEAOKLLGLMGIPYIAPTAEAAQCAELAKKGVYAAASEMDTLCYRTPFLLRHLTFSEAKKEPIH						YST510.PRO
50	KEVOELLSRFGIPYITAPMEAAQCAELQLNLVDGII TDDSDVFLFGGTYKVMFHEKNY----VE						YSTRAD2.PRO
55	KECOELLRLFGIPYIVAPOEAAQCSKLLLEKLVDGIVTDDSDVFLFGGTRVYRNMFNONKF----VE						SPORAD13.PRO
60	FELESCELLRLFGIPYIOAPMEAAQCAILDLTDOTSGTITDDSDIWLFGARHVYRNFNKNKF----VE						HUMXPG.PRO
65	FELESOELLRLFGIPYIOAPMEAAQCAVLDLSDOTSGTITDDSDIWLFGARHVYKNNFNKNKF----VE						MUSXPG.PRO
70	FELESOELLRLFGIPYIVAPMEAAQCAILDLTDOTSGTITDDSDIWLFGARHVYKNNFNKNKF----VE						XENXPG.PRO
75	FELESOELLRLFGIPYIVAPMEAAQCAILDLTDOTSGTITDDSDIWLFGARHVYKNNFNKNKF----VE						CELRAD2.PRO

	220	230	240	250	260	270	280
80	PELIELNEVLEDRLISLDLIDIAIFMGTOYNPGGV--K--GIGFKRAYELVRSGVAK--DV						MJAFEN1.PRO
85	VE-IXPELILEEVKLKLTREKLIELAILVGTOYNPGGI--K--GIGLKKALEIVRHSKOPLAKF						PFUFEN1.PRO
90	LSRILOEGLNOEOFVOLCILLGSDYCESIRGIGKRAVDL IOK--HKSIEEIVRRLDPN--K--KY						HUMFEN1.PRO
95	LSRVLGELGNOEOFVOLCILLGSDYCESIRGIGAKRAVDL IOK--HKSIEEIVRRLDPS--K--KY						MUSFEN1.PRO
100	IELVLRGLDTIEQFVOLCIMLGSDYCESIRGVGPVLTALKIKT--HGSIEKIVEFIESGESNNTKW						YST510.PRO
105	DAESILKLILGDRKNMIELAQLLGSDYINGLKMGMPVSSIEVIAEF--GNLKNFKOWYNNNGQFDKRX						YSTRAD2.PRO
110	MDMKREFNVNOMDLIKLAHLLGSDYTMGLSRVGPVLALEILHEFPOTGLFEFKKWFQRLSTGHAS						SPORAD13.PRO
115	YVDFHNOGLDRNKLINLAYLLGSDYTEGIPTVGCVTAMEILNEFFPGHGLEPLLKFSWWHEAOKNP						HUMXPG.PRO
120	YVDFYSOLGLDRNKLINLAYLLGSDYTEGIPTVGCVTAMEILNEFFPGRGLDPLLKFSWWHEAOKNP						MUSXPG.PRO
125	YVDFYSOLGLDRNKLINLAYLLGSDYTEGIPTVGVVSAMEILNEFFPGGLEPLVKFKEWWSEAOQDK						XENXPG.PRO
130	YVDFYSOLGLDRNKLINLAYLLGSDYTEGIPTVGVVSAMEILNEFFPGGLEPLVKFKEWWSEAOQDK						CELRAD2.PRO

[illegible]

	360	370	380	390	400	410	420
N	LYNLIA						N
F	LKKA						F
H	LSKSROGS	-TQRLDFFKVT-					H
N	LSKSROGS	-TQRLDFFKVT-					N
Y	LKKGLKSG	-TQRLDGGFOVV-					Y
Y	LIRDVNRKK						-KGKO
S	YIQDWHKKOF						-VGTO
F	WYLCOLDAAO	TOLRIDSF	FRLAOEKE	DAKRIKSOR	LNRAV	TCMLRKEKE	AAASEIEAVSVAM
N	WYWKHLNAHO	TOLRIDSF	FRLAOEKE	KODAKLIKSHR	LSRAV	TCMLRKERE	EKAPELTKVTEAM
X	WYKOLNAO	TOLRIDSF	FRLAOEKE	HEAAG--	-LKSOR	LRRAV	TCMKRKEROVEAE
C	WYKOLNAO	TOLRIDSF	FRLAOEKE	HEAAG--	-LKSOR	LRRAV	TCMKRKEROVEAE

[REDACTED]

SECRET

74

MJAFEN1.PRO
PFUFEN1.PRO
HUMFEN1.PRO
MUSFEN1.PRO
YST510.PRO
YSTRAD2.PRO
SPORAD13.PRO
HUMXPG.PRO
MUSXPG.PRO
XENXPG.PRO
CELRAD2.PRO

122	WFKZ
123	WFKR
124	WFKK
125	WFRK
126	WKRK
127	WRRK
128	WRRK
129	WRTZ
130	WRTK
131	WRRK

7k

FIGURE 60

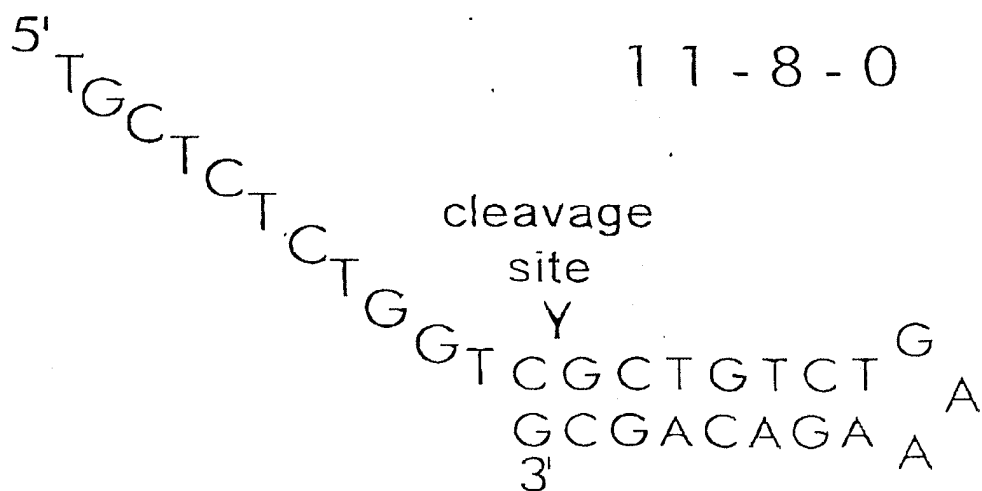
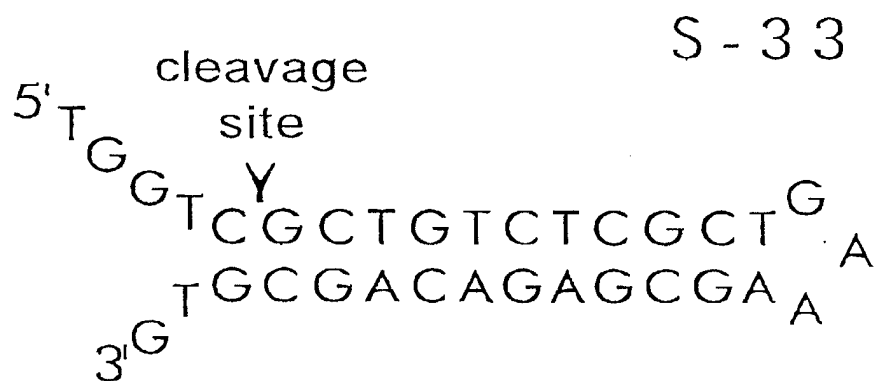


FIGURE 62

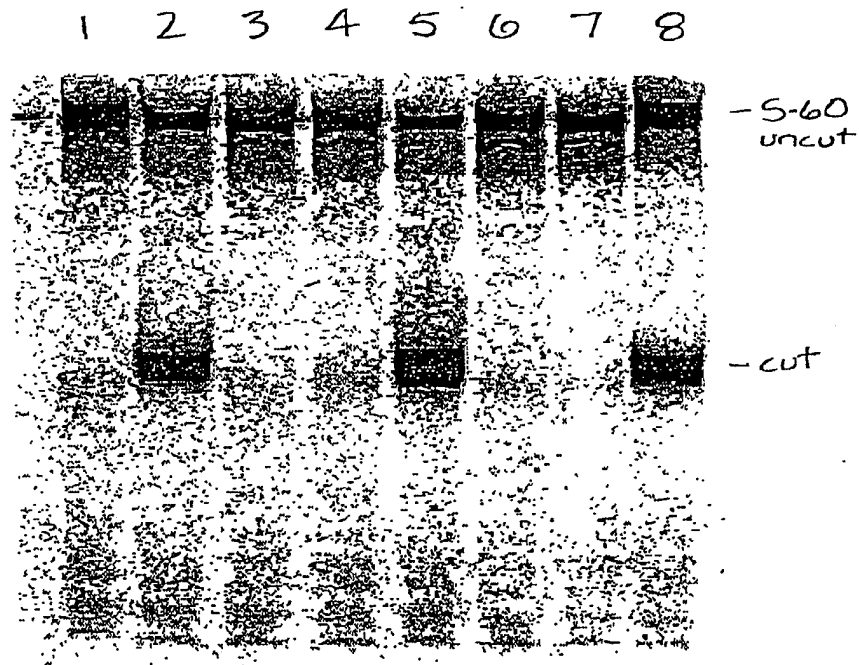
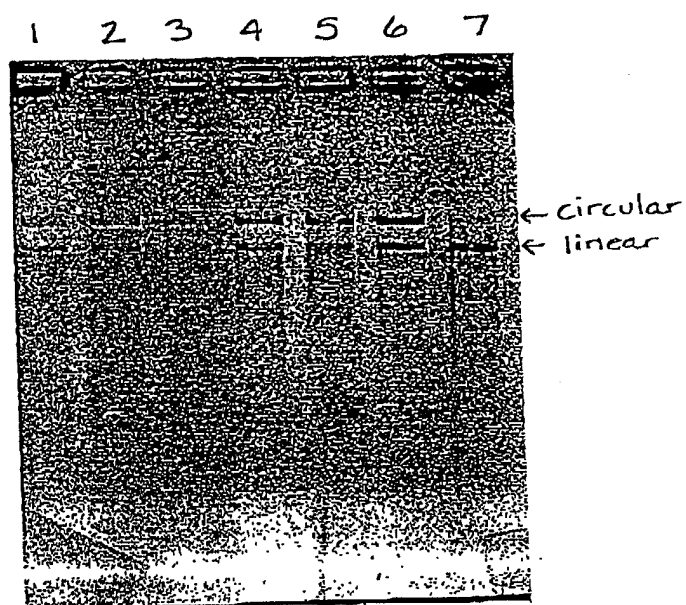


FIGURE 63



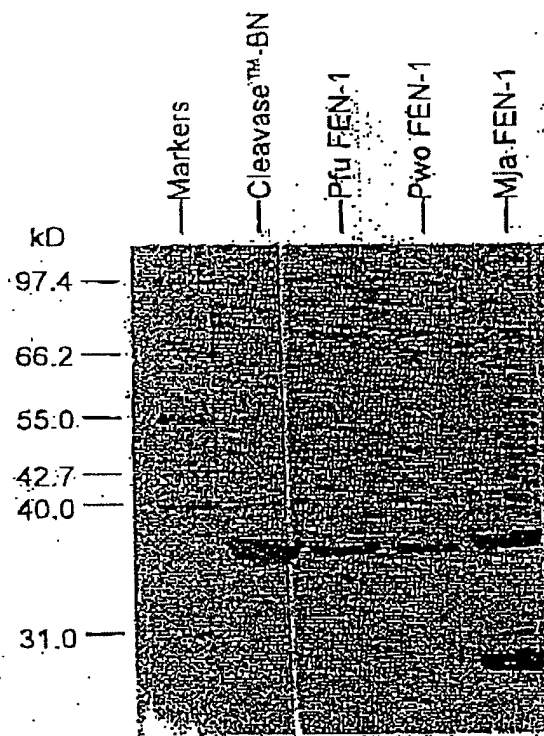


FIGURE 64

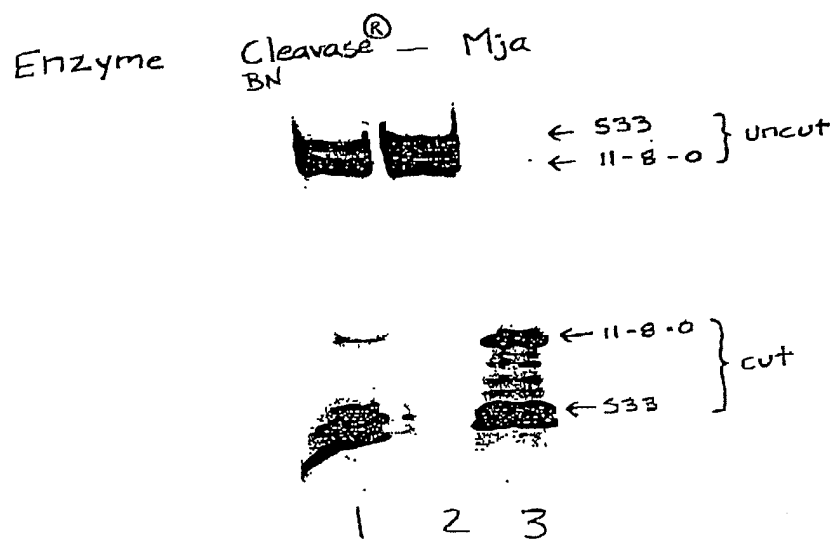


FIGURE 65

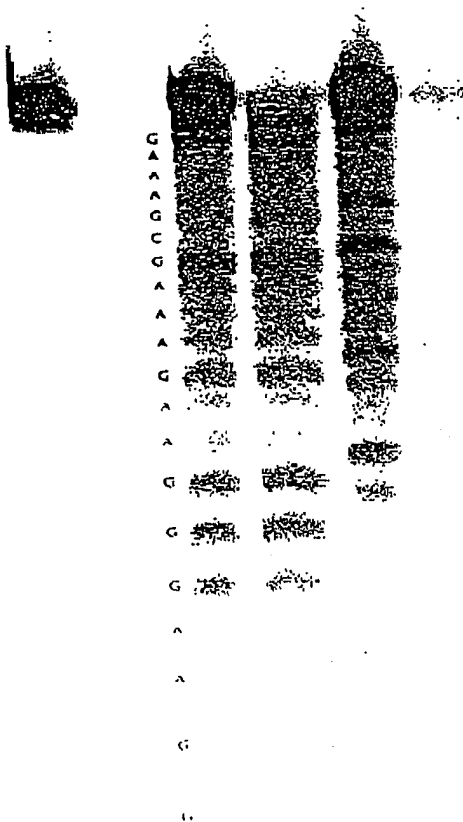
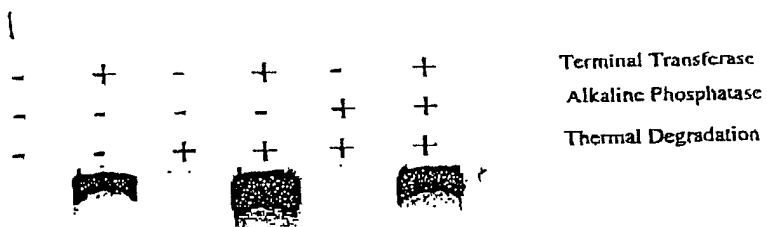


FIGURE 66

5'-nAGAAAggaaggga agaaagcgaaagG-3'

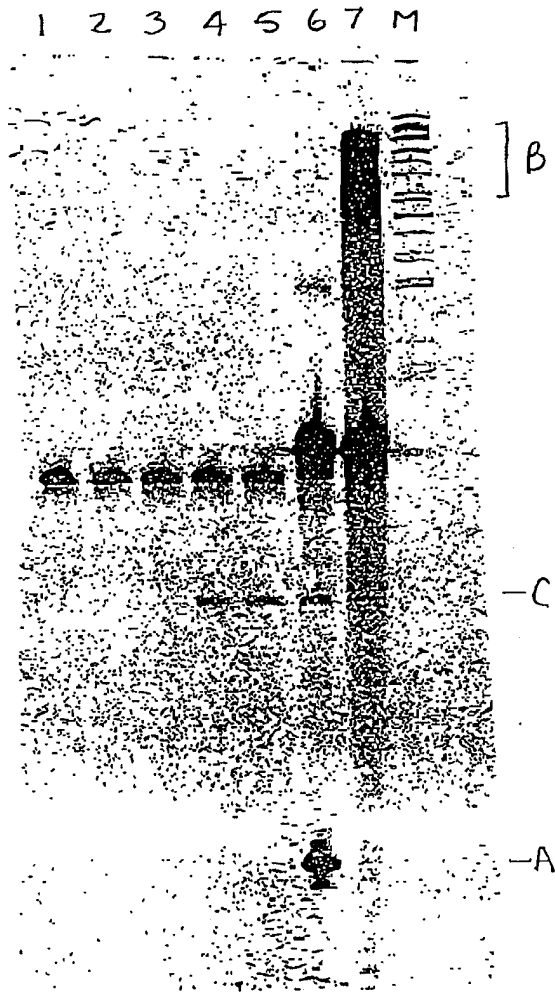


FIGURE 67

FIGURE 68

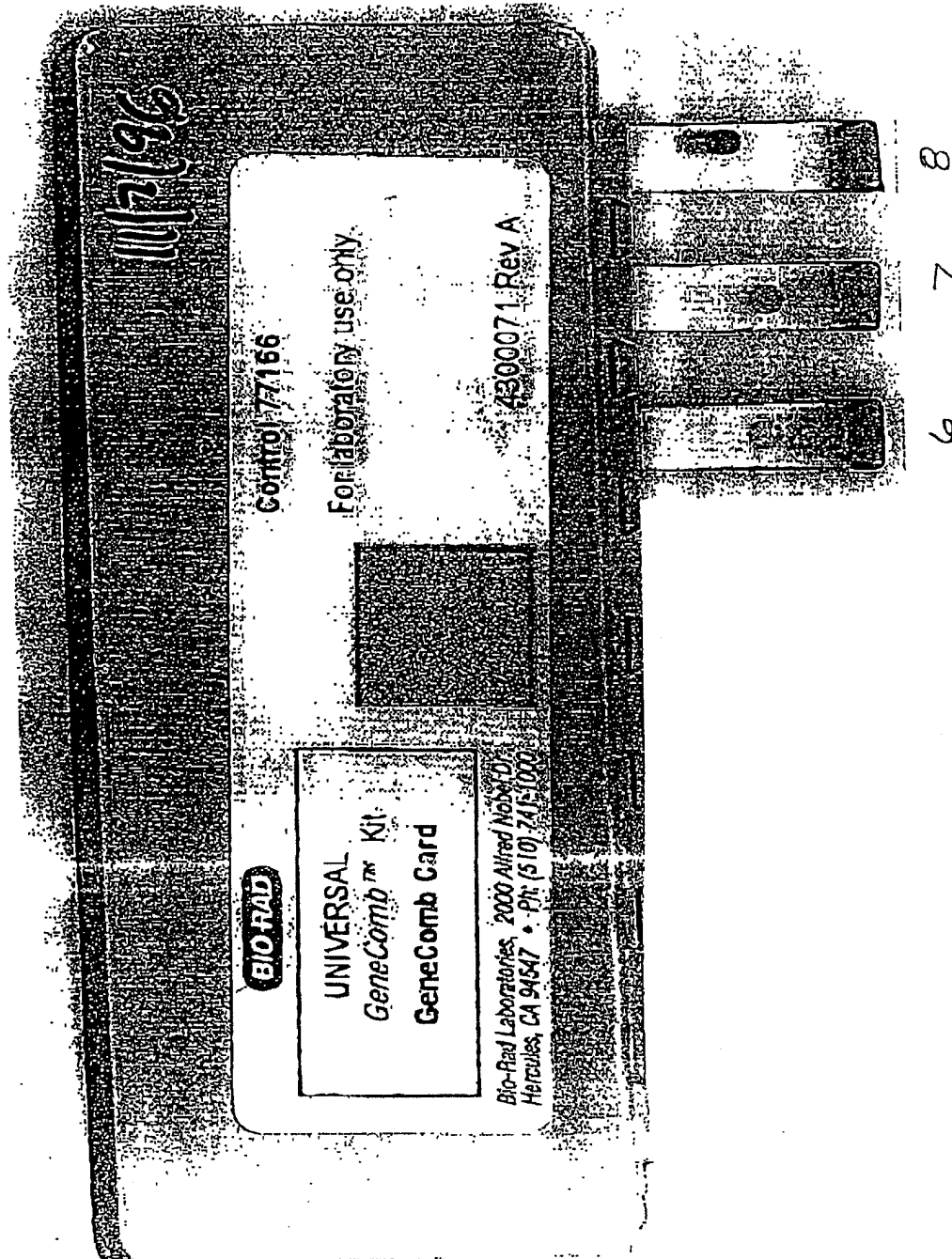
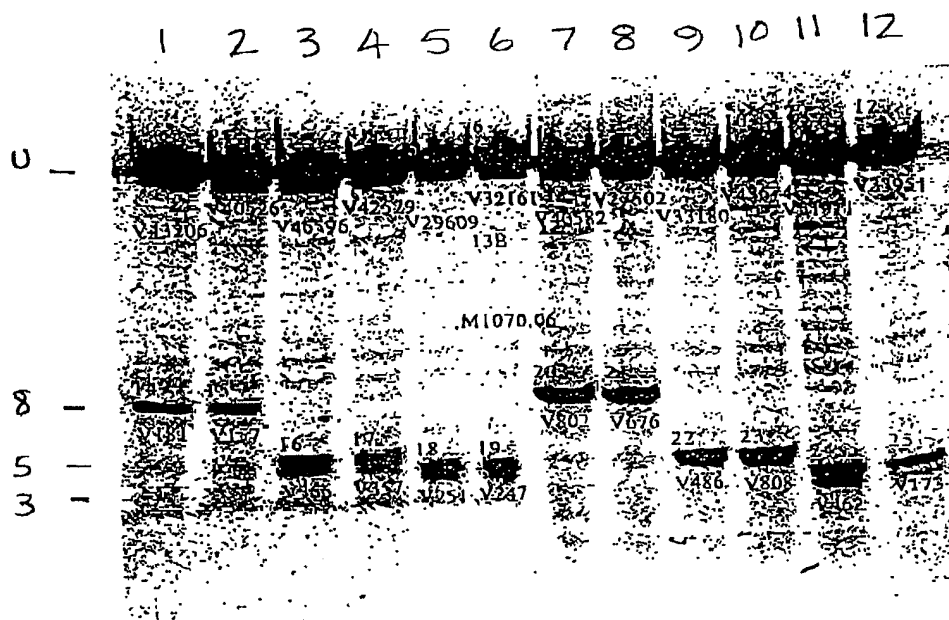


FIGURE 69



85

A

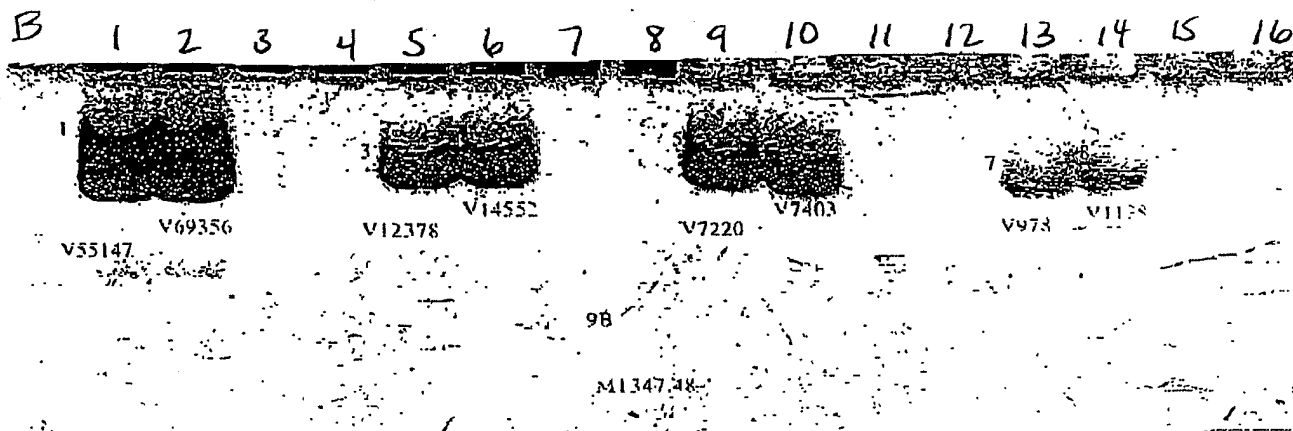
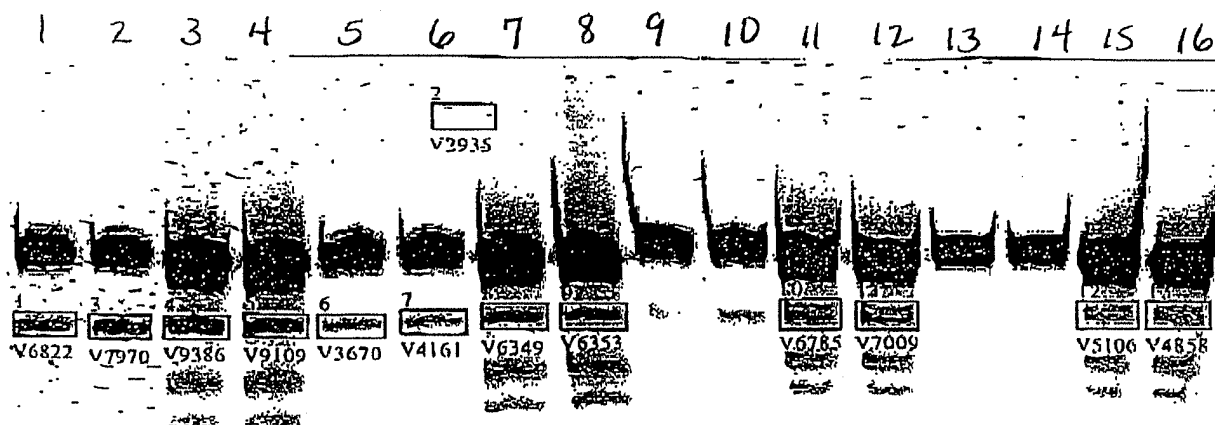
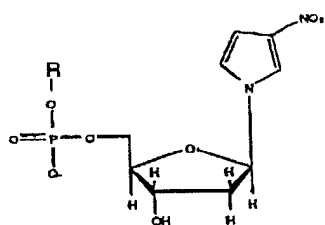
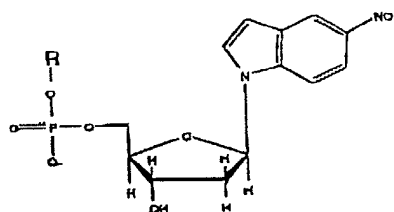


FIGURE 72

FIGURE 73**3-nitropyrrole****5-nitroindole**

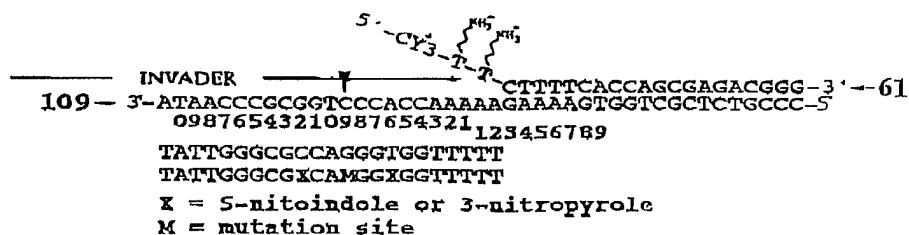
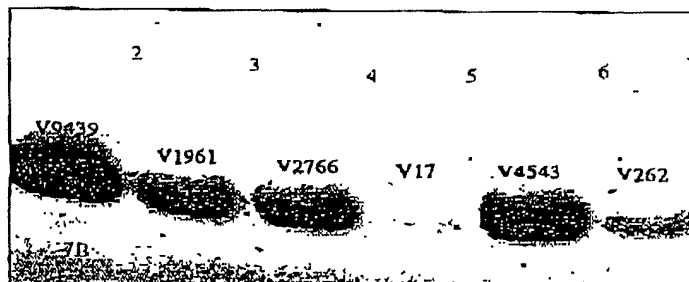


FIGURE 74

	All Comp	1 Base Mismatch	All Comp	1 Base Mismatch	All Comp	1 Base Mismatch
	2 NI	2 NI	1 NP	1 NP	1 NP	1 NP
Invent #	67	114	115	116	112	113

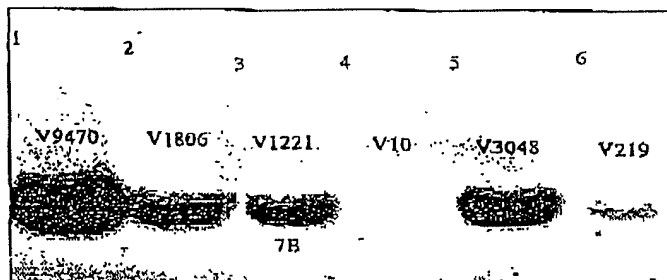
A

52°C



B

55°C



C

58°C

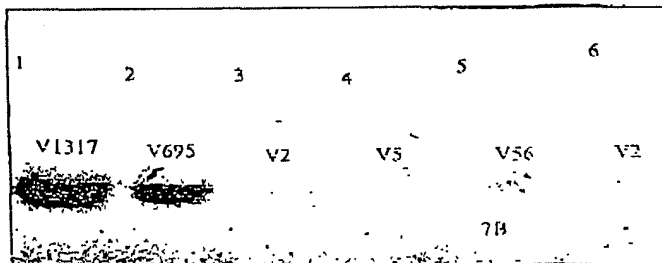


FIGURE 75

FIGURE 76

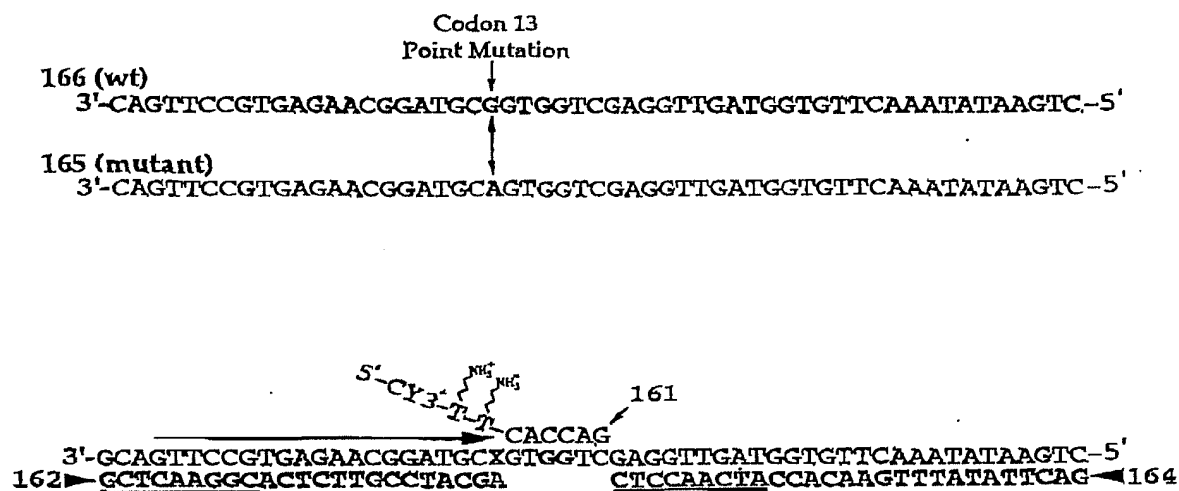
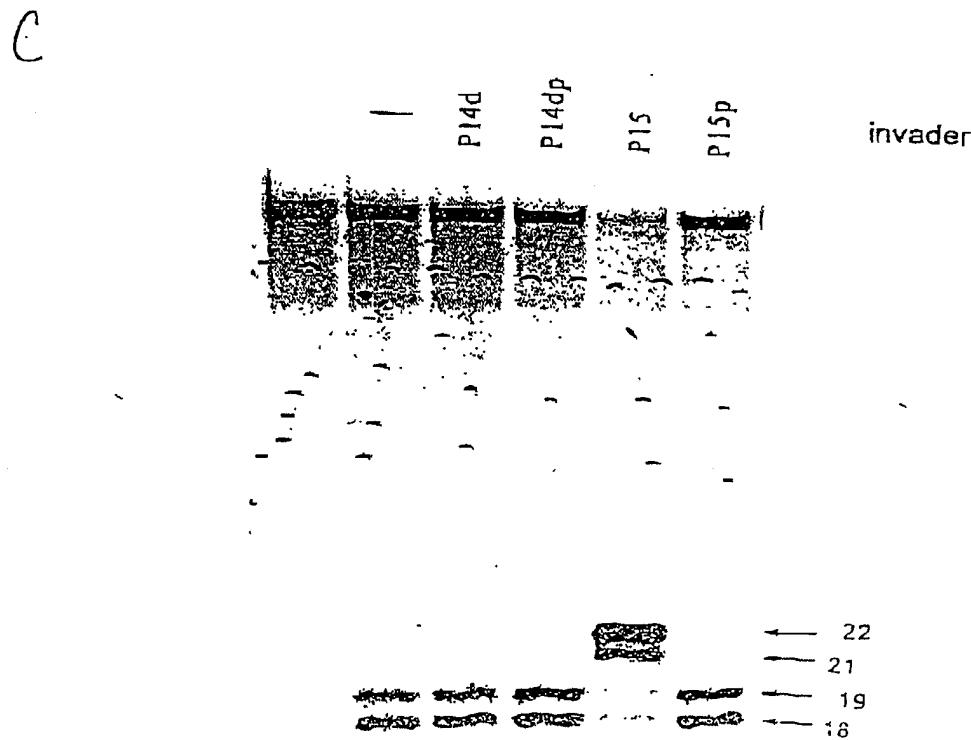
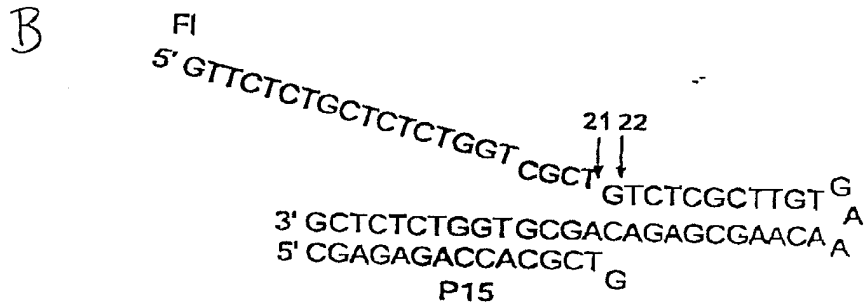
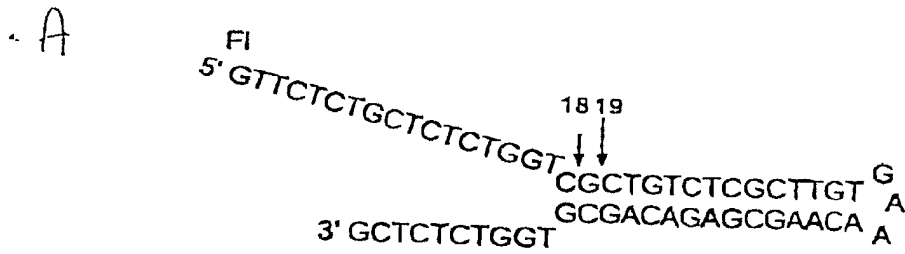


FIGURE 77

Temp	→		47°		50°		53°		56°	
Target	→	—	165	166	165	166	165	166	165	166



FIGURE 78



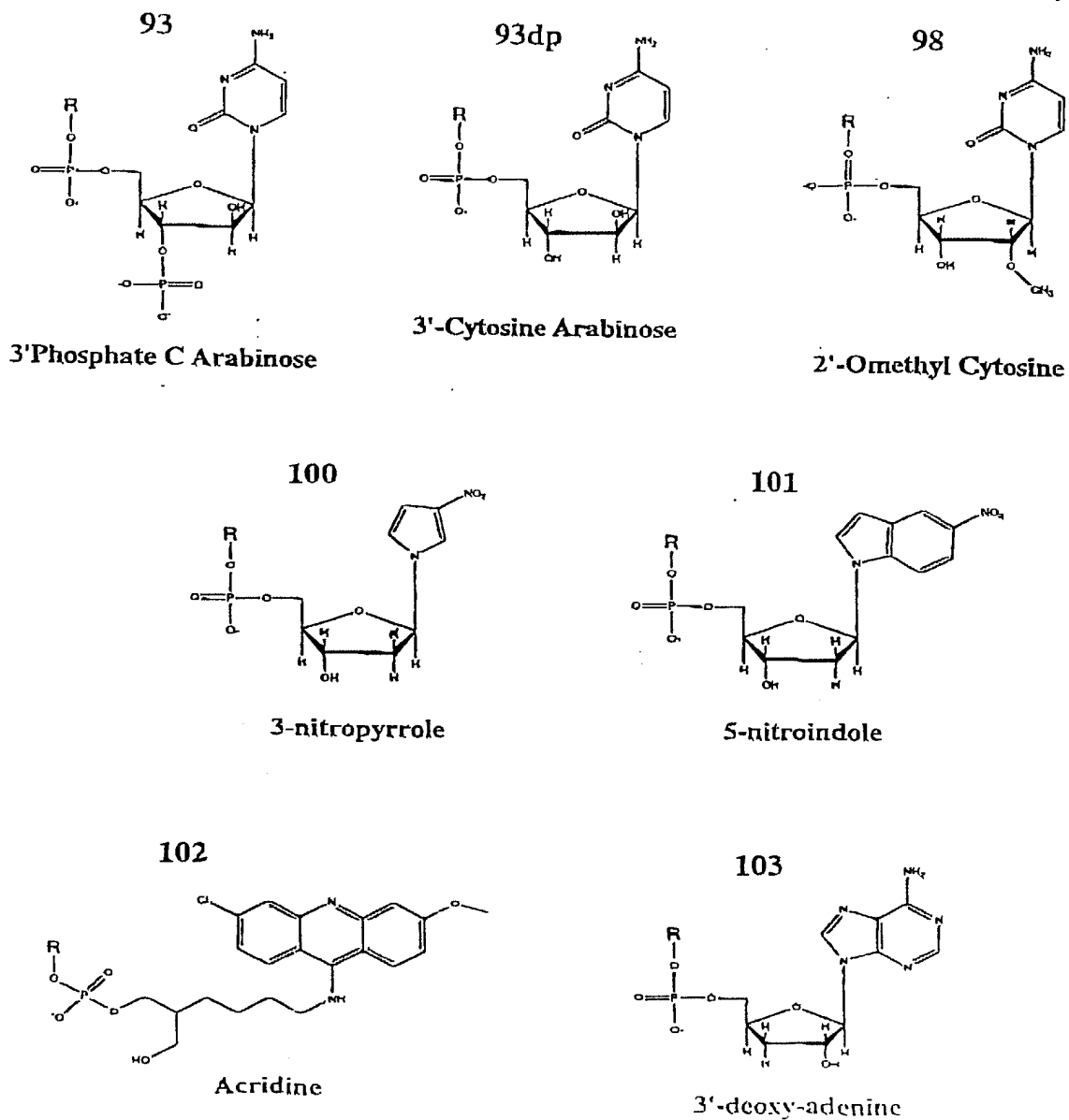


FIGURE 79

95

Concentration of Probe w/ and w/o Stacker vs Temp

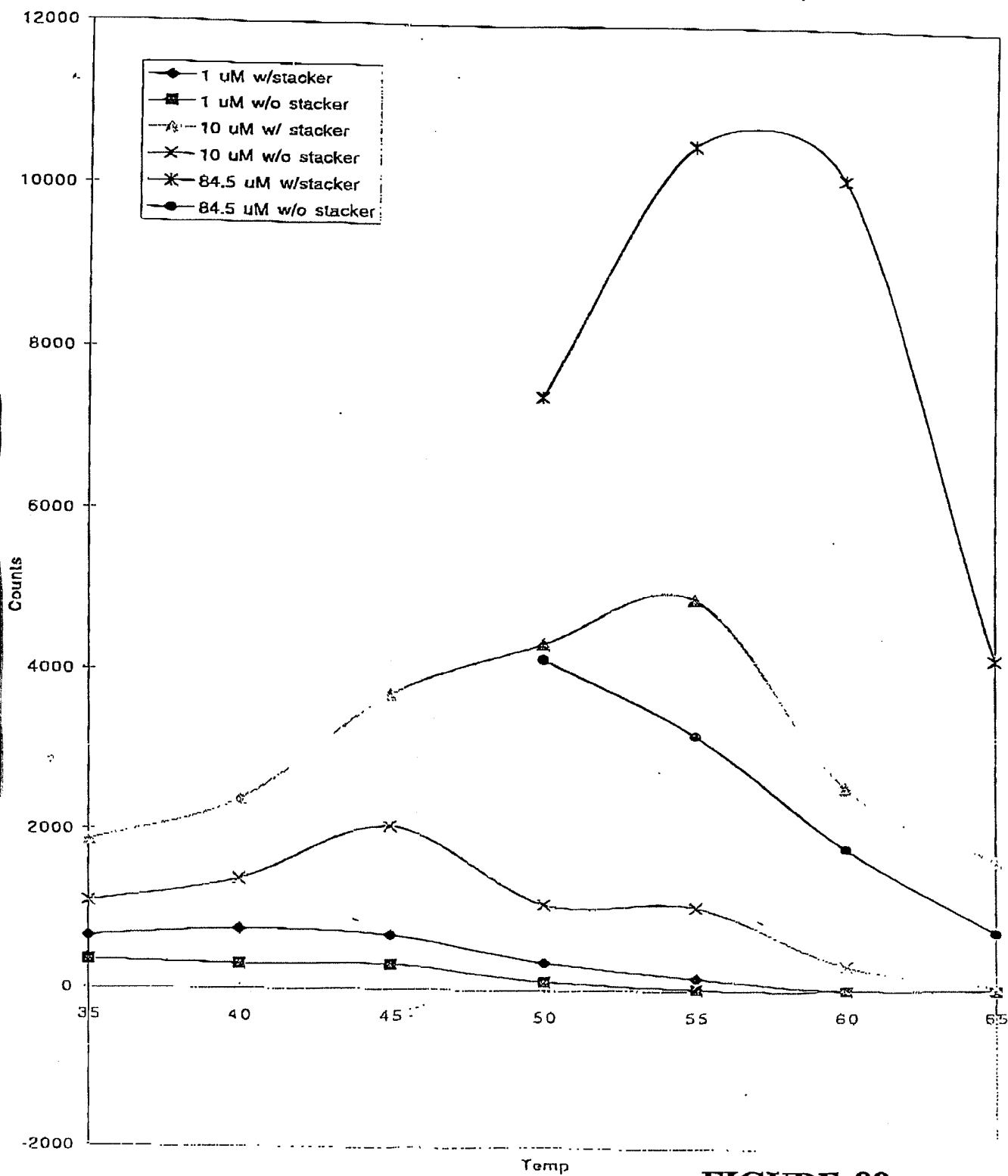


FIGURE 80

FIGURE 81

cleavage
site

IT-2

5' T TTTCCAGAGCCCTAAT^G A
3' GTGCTCGCAGAAAGGTCCTCGGATTA^A
5' AACGAGCGTCTTTG3'

IT-1

cleavage
site

IT-2

5' T TTTCCAGAGCCCTAAT^G A
3' GTGCTCGCAGAAAGGTCCTCGGATTA^A
5' AACGAGCGTCATTG3'

IT-1A4

FIGURE 82

1 2 3 4



-Uncut

FIGURE 83

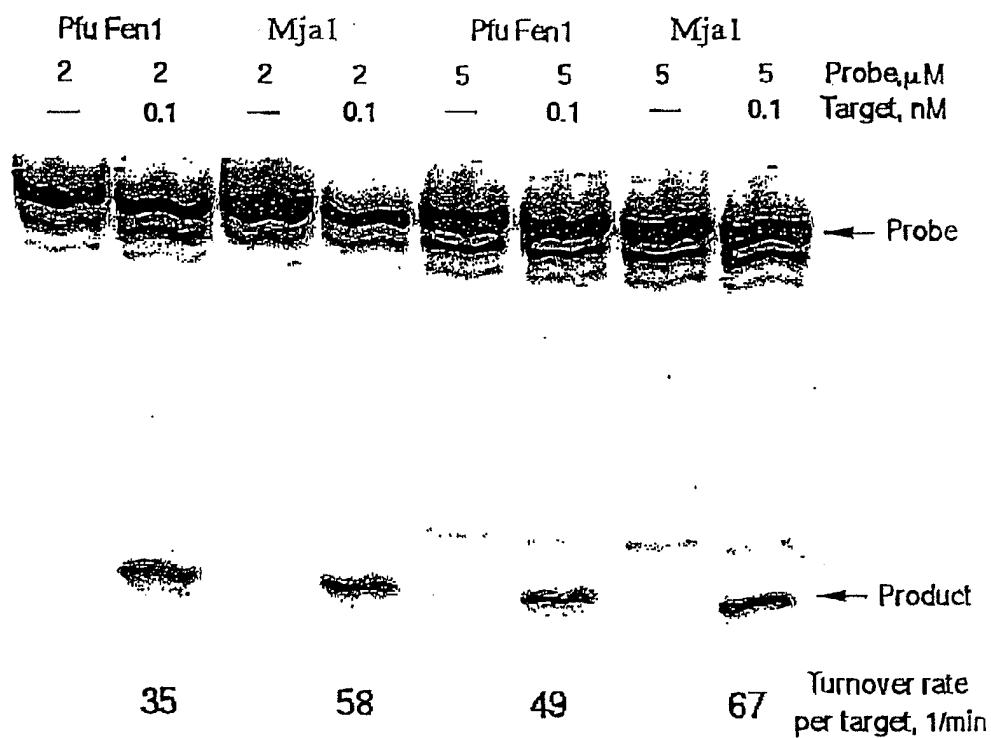


FIGURE 84

1 2 3 4 5

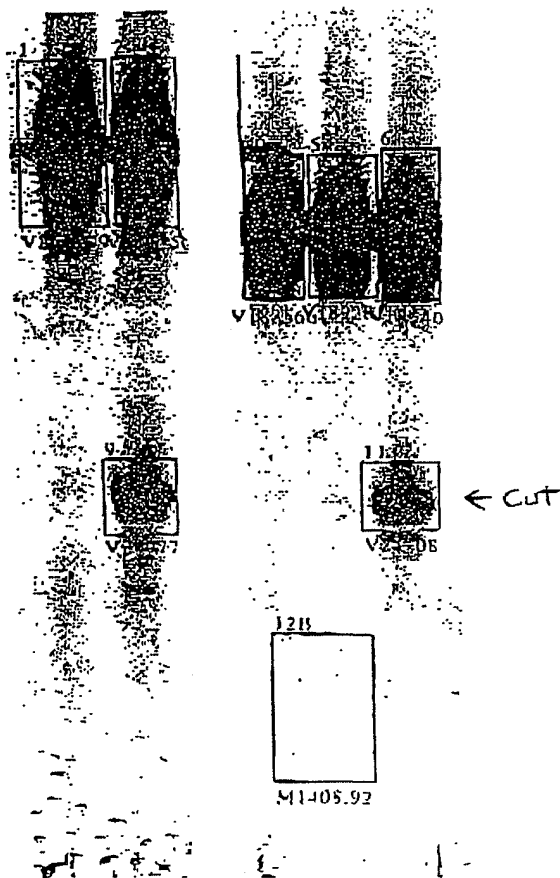
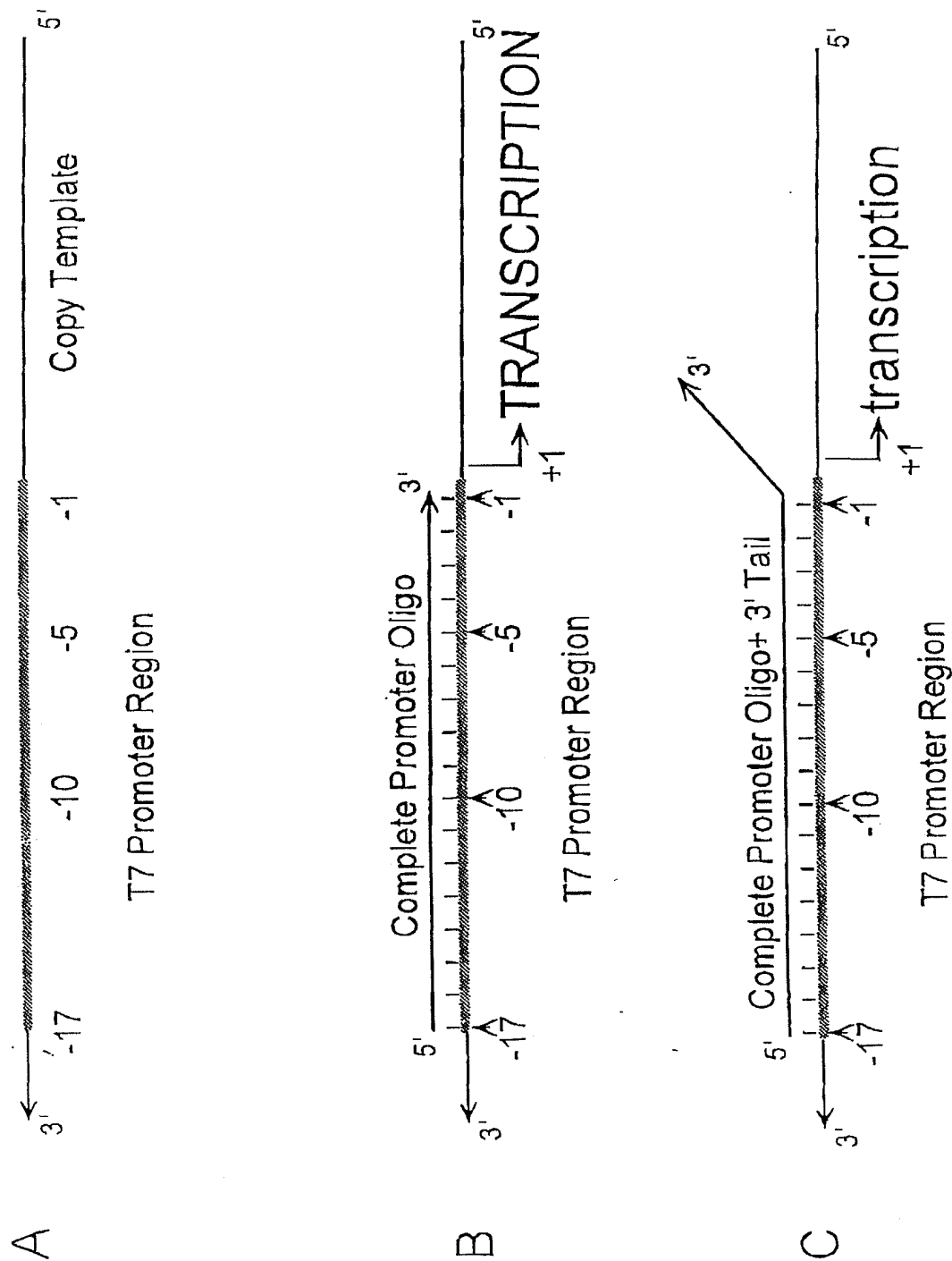


FIGURE 85



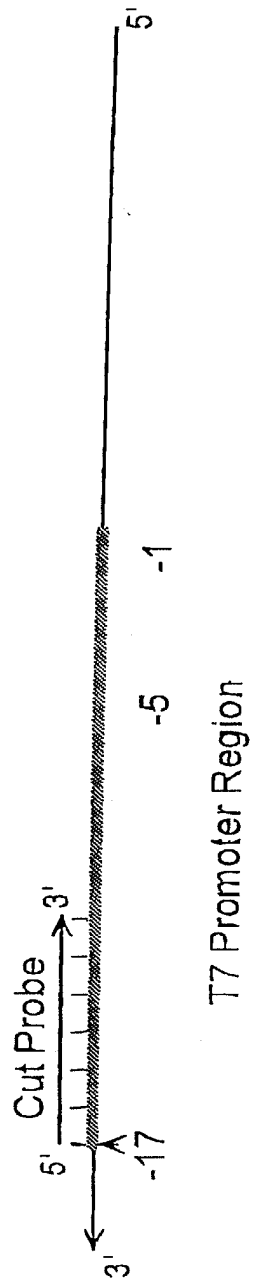


FIGURE 86A

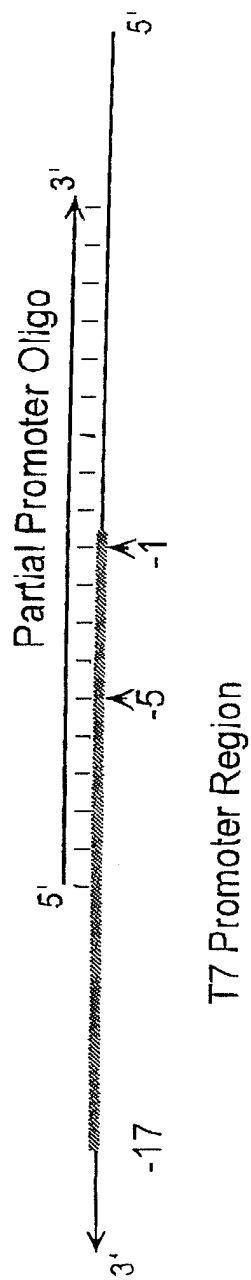


FIGURE 86B

FIGURE 87

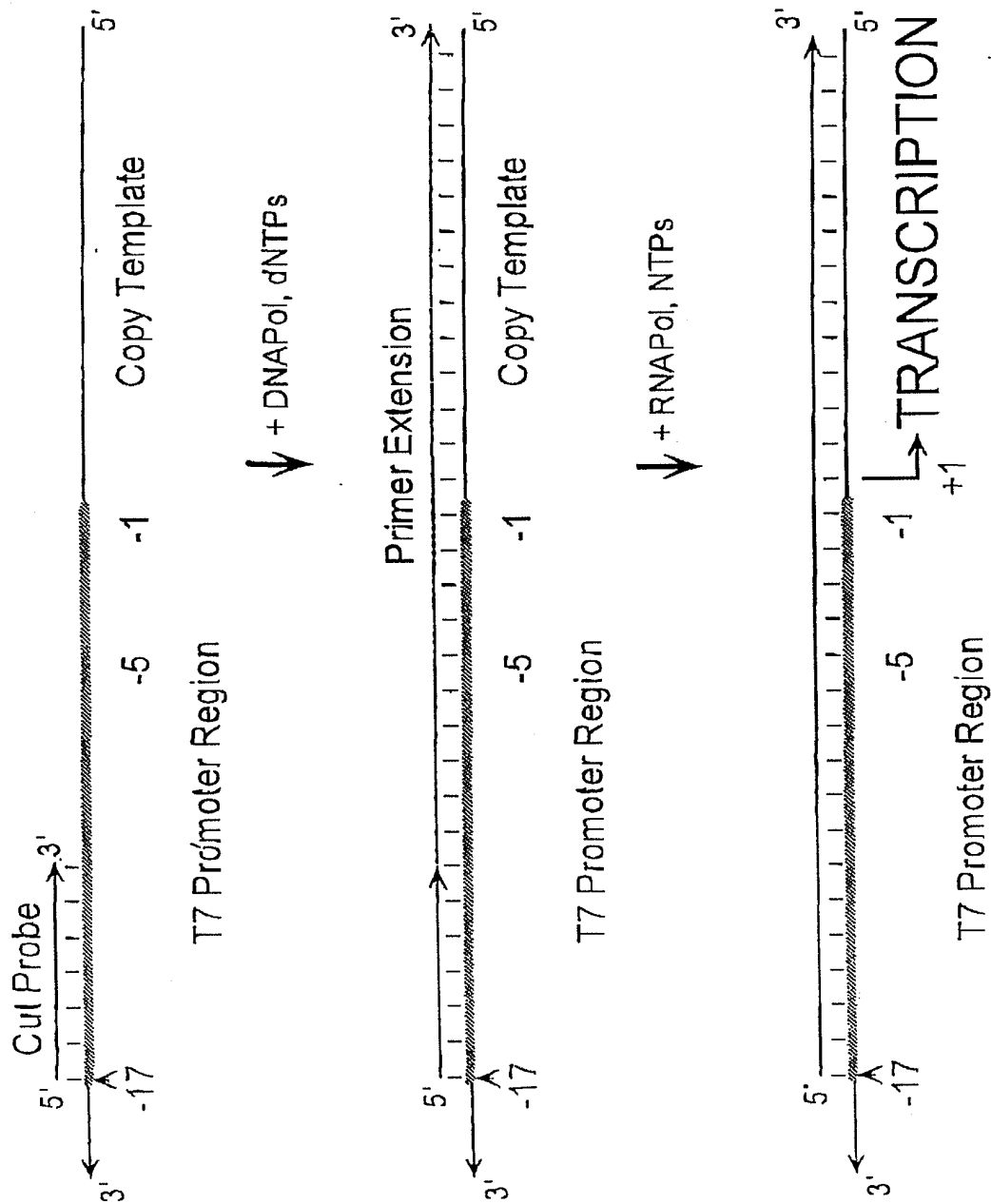


FIGURE 89

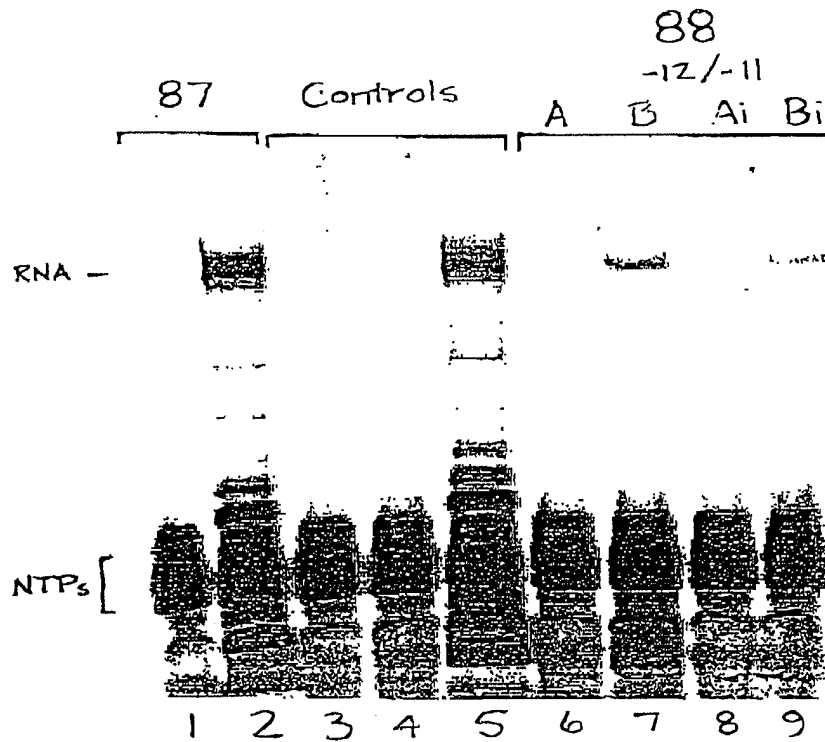
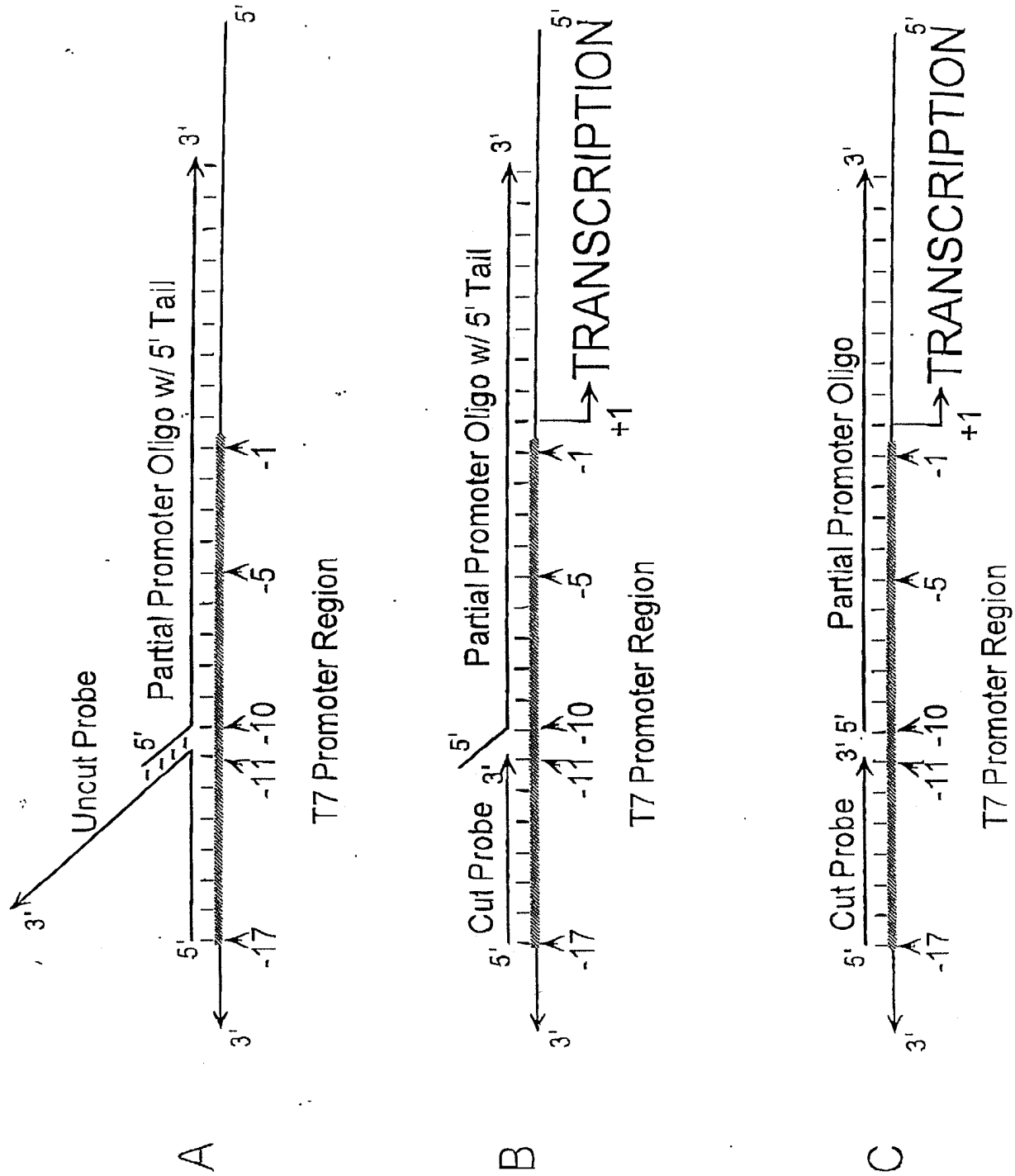


FIGURE 90



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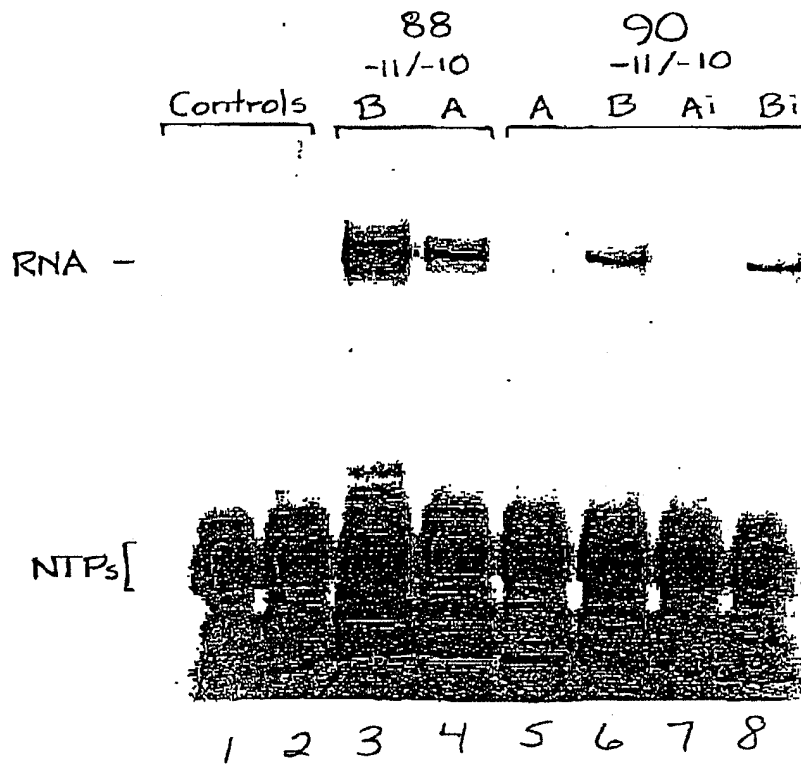


FIGURE 91

FIGURE 92

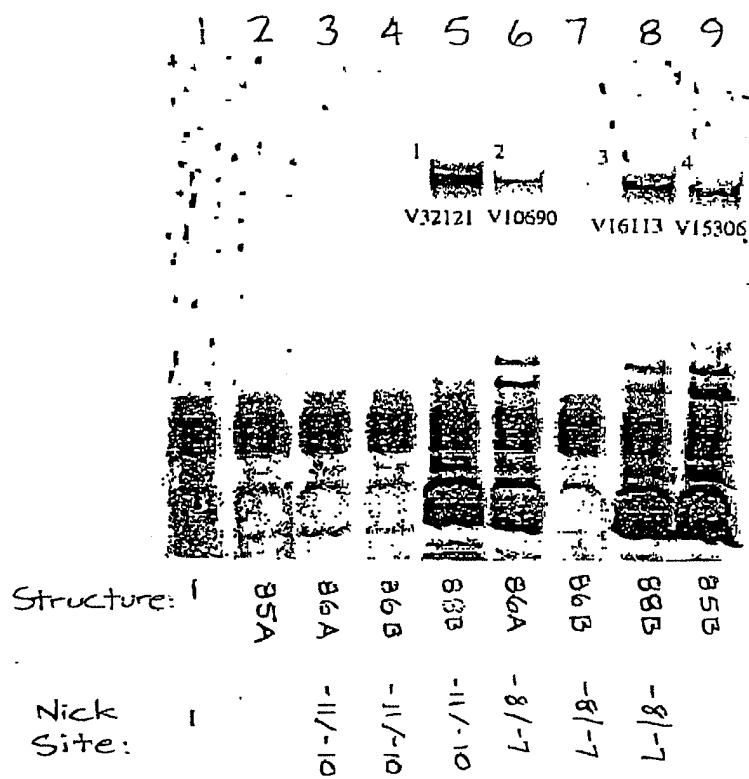
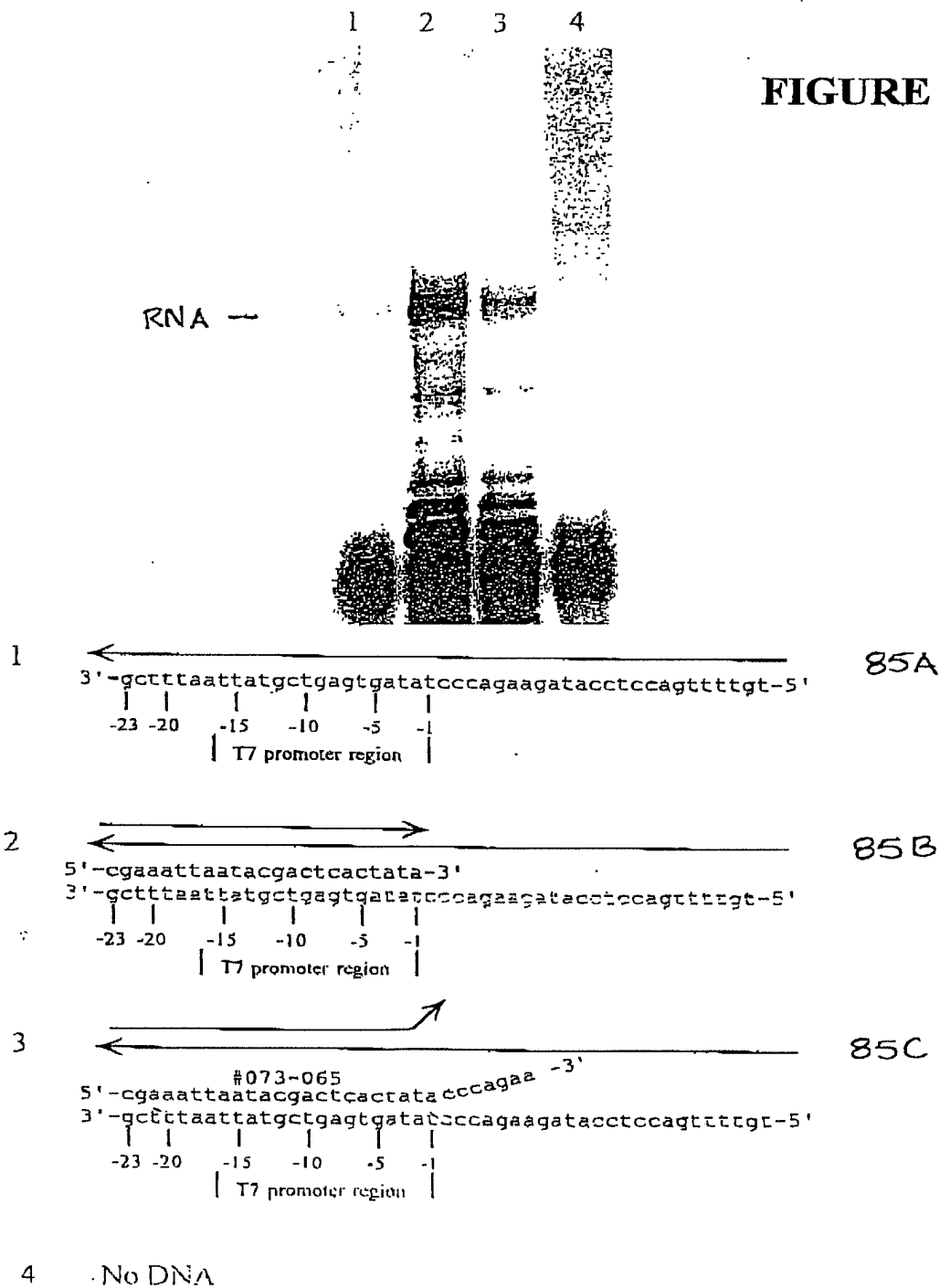


FIGURE 93



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FIGURE 94

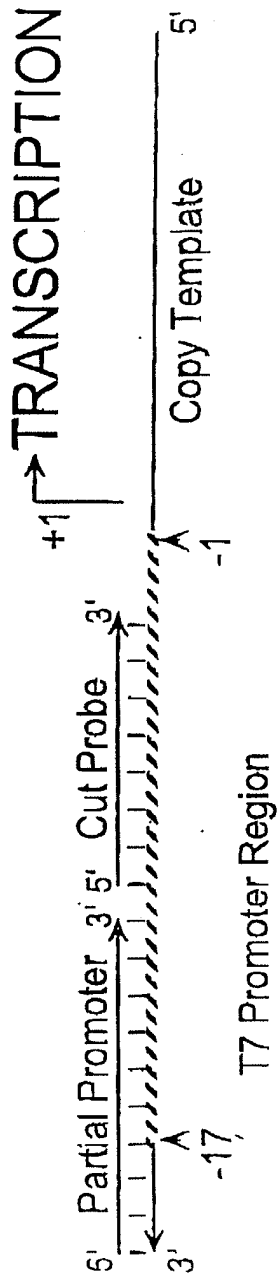


FIGURE 95A

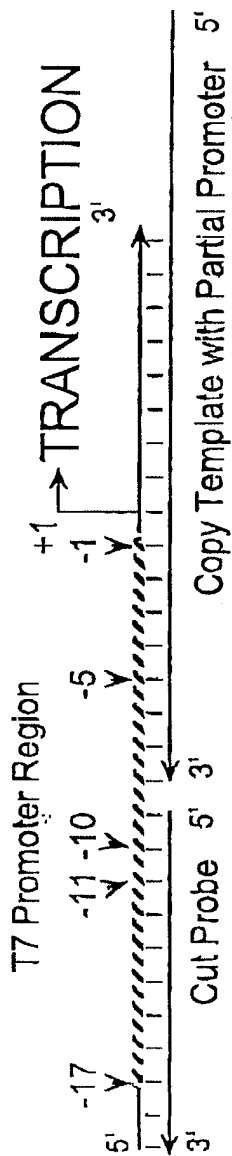


FIGURE 95B

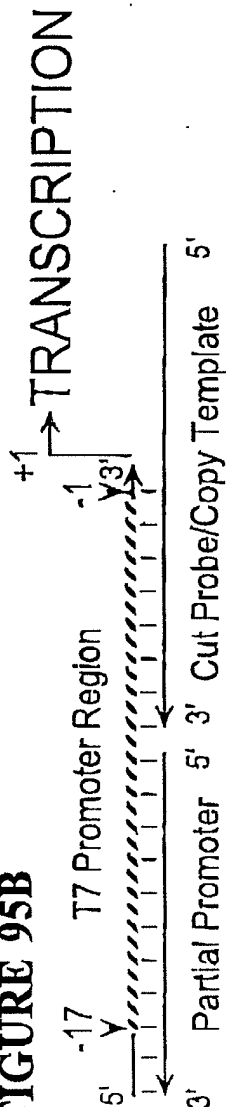


FIGURE 95C

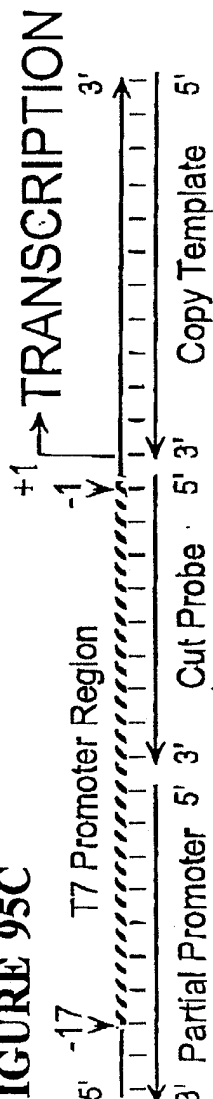
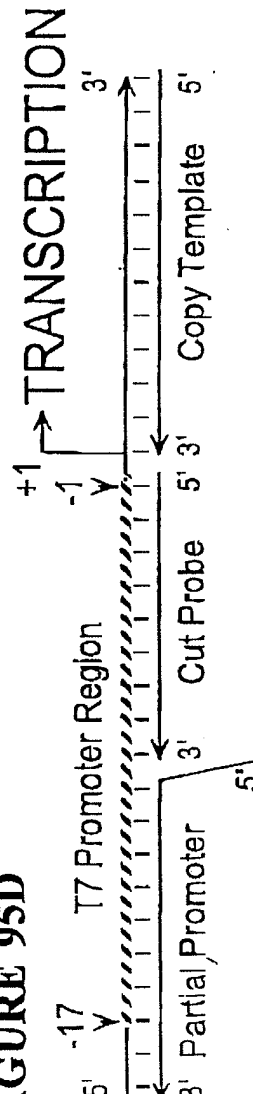


FIGURE 95D



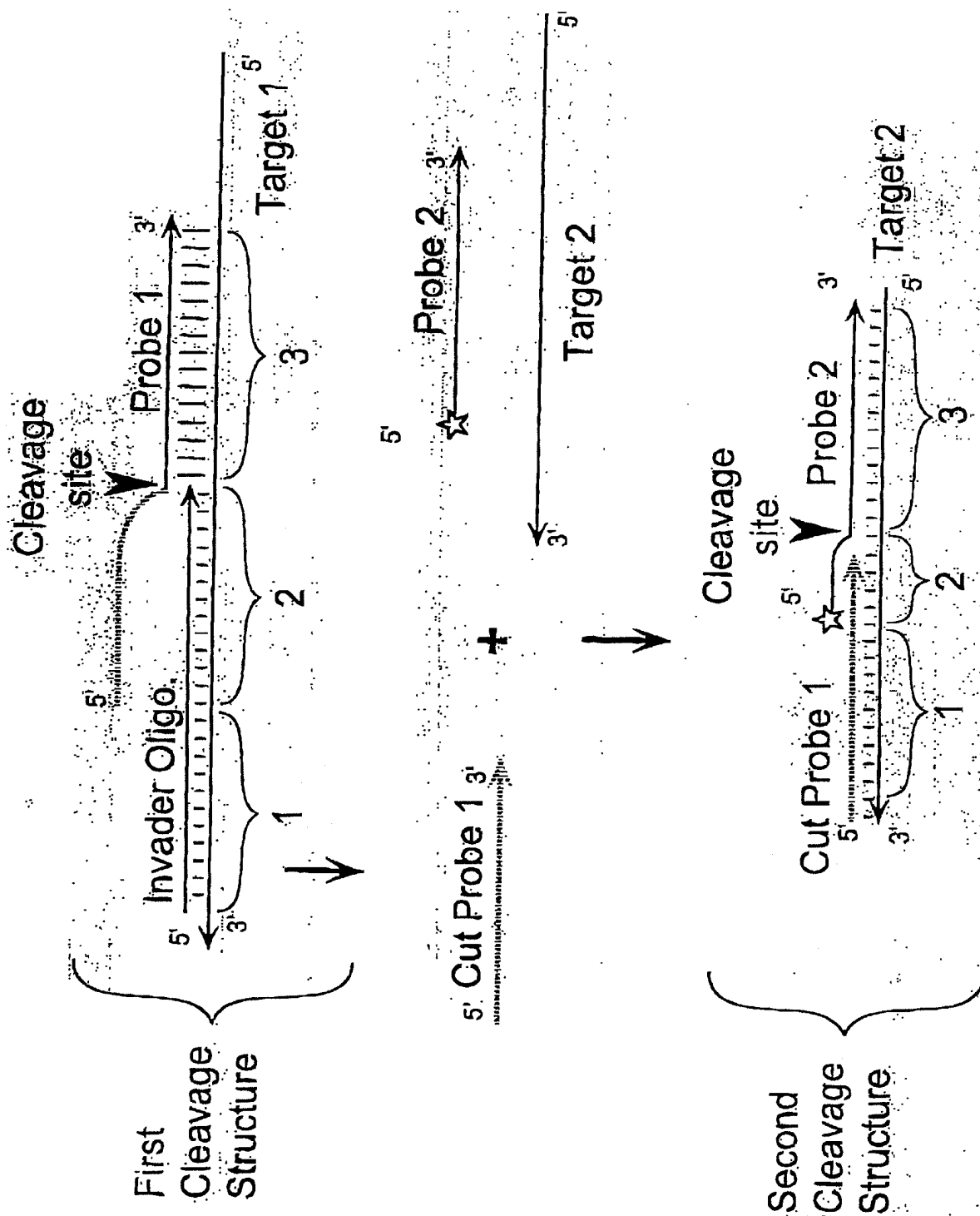
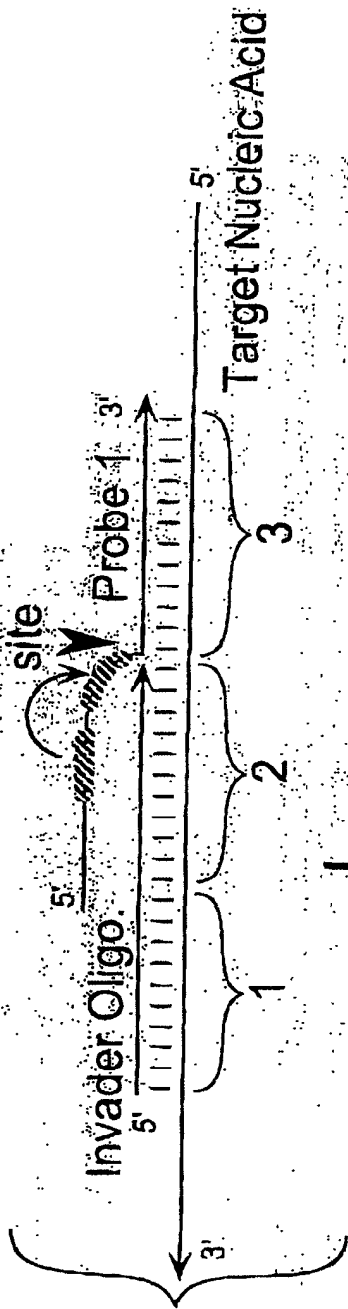
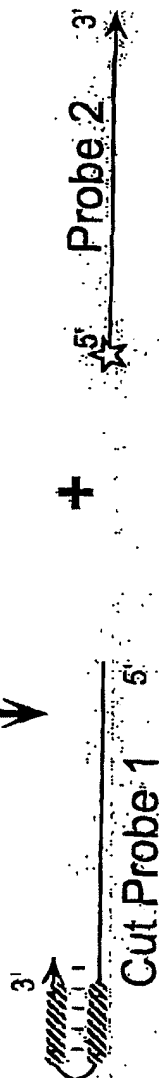
FIGURE

FIGURE 1

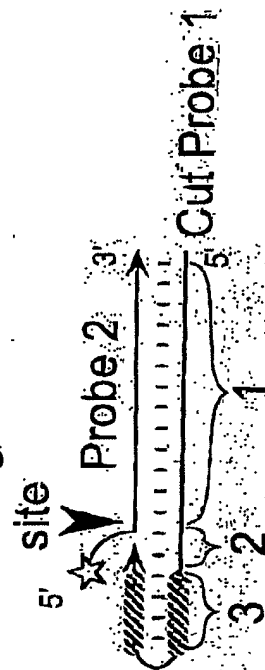
Cleavage site



First
Cleavage
Structure



Cleavage site



Second
Cleavage
Structure

FIGURE 100

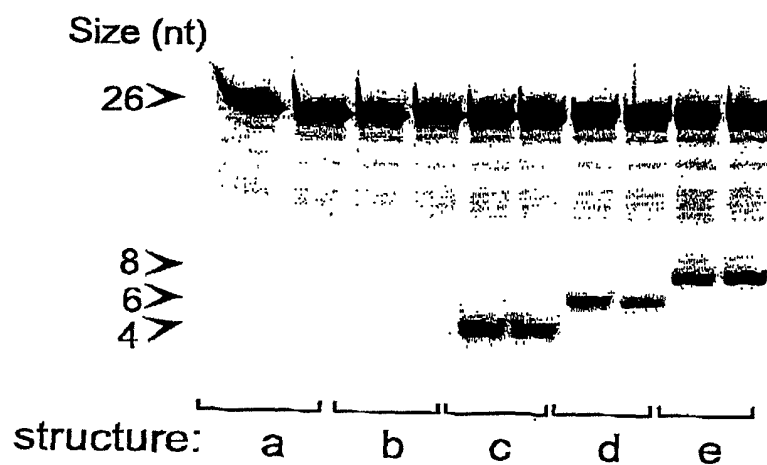
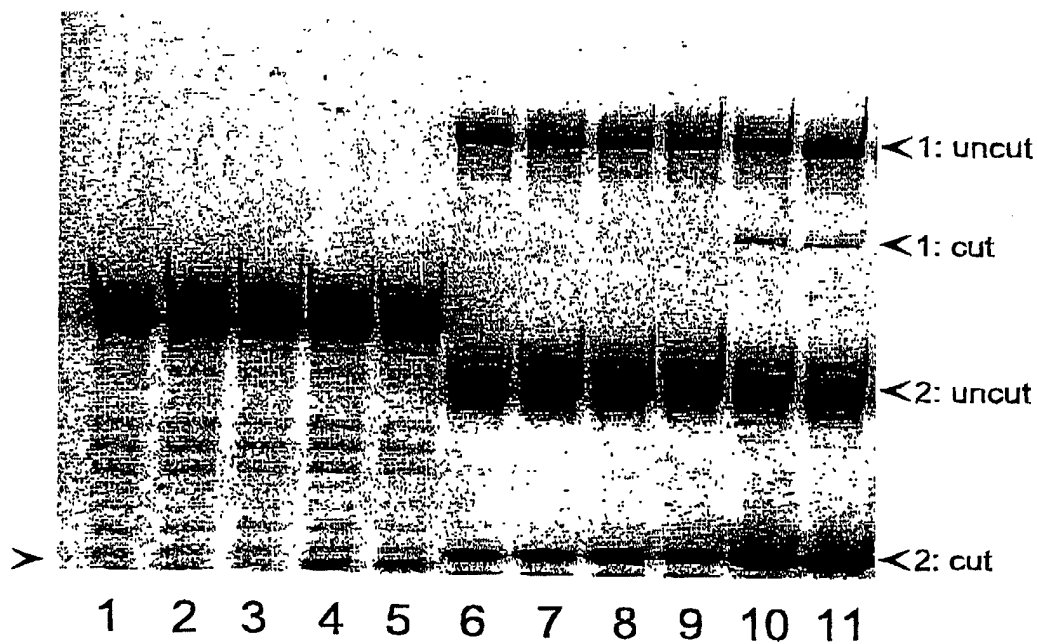


FIGURE 101

a



b

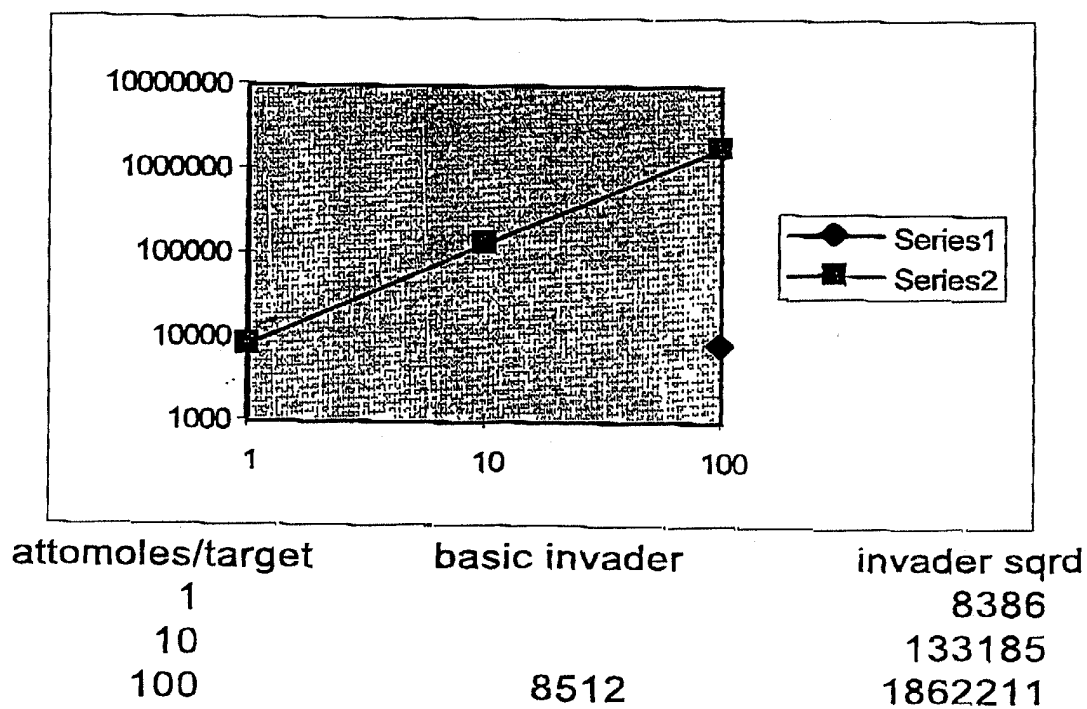


FIGURE 102

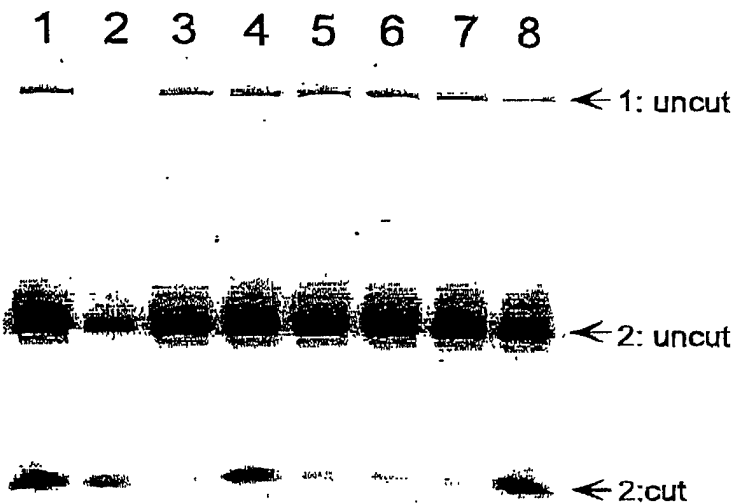
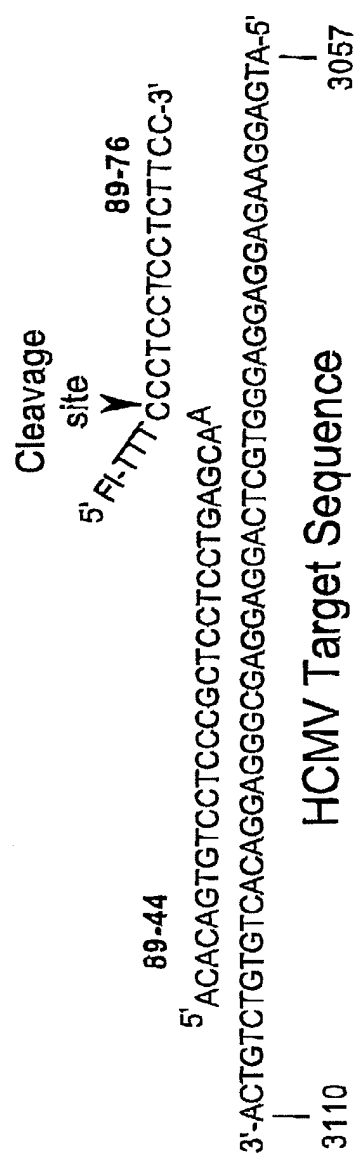


FIGURE 103



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FIGURE 104

